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(54) Title: METHODS AND COMPOSITIONS FOR ENHANCING THE EFFICACY AND SPECIFICITY OF FNAi

(57) Abstract: The present invention provides methods of enhancing the efficacy and specificity of RNAi. The invention also provides compositions for mediating RNAi. In particular, the invention provides siRNAs, shRNAs, vectors and transgenes having improved specificity and efficacy in mediating silencing of a target gene. Therapeutic methods are also featured.

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METHODS AND COMPOSITIONS FOR ENHANCING THE EFFICACY AND SPECIFICITY OF RNAi

Government Rights

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Related Applications

This patent application claims the benefit of U.S. Provisional Patent Applications Serial No. 60/475,331, entitled "Methods and Compositions for Enhancing the Efficacy and Specificity of RNAi," filed June 2, 2003; U.S. Provisional Patent Application Serial No. 60/507,928 entitled "Methods and Compositions for Enhancing the Efficacy and Specificity of RNAi," filed September 30, 2003; and U.S. Provisional Patent Application Serial No. 60/XXXXXX entitled "Methods and Compositions for Enhancing the Efficacy and Specificity of RNAi," filed May 28, 2004 and bearing attorney docket number UMY-066-3. The entire contents of the above-referenced provisional patent applications are incorporated herein by this reference.

Background of the Invention

Two types of ~21 nt RNAs trigger post-transcriptional gene silencing in animals: small interfering RNAs (siRNAs) and microRNAs (miRNAs). Both siRNAs and miRNAs are produced by the cleavage of double-stranded RNA (dsRNA) precursors by Dicer, a of the RNase III family of dsRNA-specific endonucleases (Bernstein et al.,2001; Billy et al., 2001; Grishok et al., 2001; Hutvágner et al., 2001; Ketting et al., 2001;Knight and Bass, 2001; Paddison et al., 2002; Park et al., 2002; Provost et al., 2002;Reinhart et al., 2002; Zhang et al., 2002; Doi et al., 2003; Myers et al., 2003). siRNAs result when transposons, viruses or endogenous genes express long dsRNA or when dsRNA is introduced experimentally into plant or animal cells to trigger gene silencing, a process known as RNA interference (RNAi) (Fire et al., 1998; Hamilton and Baulcombe, 1999; Zamore et al., 2000; Elbashir et al., 2001a; Hammond et al., 2001; Sijen et al., 2001; Catalanotto et al., 2002). In contrast, miRNAs are the products of

endogenous, non-coding genes whose precursor RNA transcripts can form small stem-loops from which mature miRNAs are cleaved by Dicer (Lagos-Quintana et al., 2001; Lau et al., 2001; Lee and Ambros, 2001; Lagos-Quintana et al., 2002; Mourelatos et al., 2002; Reinhart et al., 2002; Ambros et al., 2003; Brennecke et al., 2003; Lagos-Quintana et al., 2003; Lim et al., 2003a; Lim et al., 2003b). miRNAs are encoded in genes distinct from the mRNAs whose expression they control.

siRNAs were first identified as the specificity determinants of the RNA interference (RNAi) pathway (Hamilton and Baulcombe, 1999; Hammond et al., 2000), where they act as guides to direct endonucleolytic cleavage of their target RNAs (Zamore et al., 2000; Elbashir et al., 2001a). Prototypical siRNA duplexes are 21 nt, double-stranded RNAs that contain 19 base pairs, with two-nucleotide, 3′ overhanging ends (Elbashir et al., 2001a; Nykänen et al., 2001; Tang et al., 2003). Active siRNAs contain 5′ phosphates and 3′ hydroxyls (Zamore et al., 2000; Boutla et al., 2001; Nykänen et al., 2001; Chiu and Rana, 2002). Similarly, miRNAs contain 5′ phosphate and 3′ hydroxyl groups, reflecting their production by Dicer (Hutvágner et al., 2001; Mallory et al., 2002).

In plants, miRNAs regulate the expression of developmentally important proteins, often by directing mRNA cleavage (Rhoades et al., 2002; Reinhart et al., 2002; Llave et al., 2002a; Llave et al., 2002b; Xie et al., 2003; Kasschau et al., 2003; Tang et al., 2003; Chen, 2003). Whereas plant miRNA's show a high degree of complementarity to their mRNA targets, animal miRNA's have only limited complementarity to the mRNAs whose expression they control (Lee et al., 1993; Wightman et al., 1993; Olsen and Ambros, 1999; Reinhart et al., 2000; Slack et al., 2000; Abrahante et al., 2003; Brennecke et al., 2003; Lin et al., 2003; Xu et al., 2003). Animal miRNAs are thought to repress mRNA translation, rather than promote target mRNA destruction (Lee et al., 1993; Wrightman et al., 1993; Olsen and Ambross, 1999; Brennecke et al., 2003). Recent evidence suggests that the two classes of small RNAs are functionally interchangeable, with the choice of mRNA cleavage or translational repression determined solely by the degree of complementarity between the small RNA and its target (Hutvágner and Zamore, 2002; Doench et al., 2003). Furthermore, siRNAs and miRNAs are found in similar, if not identical complexes, suggesting that a single, bifunctional complex –the RNA-induced silencing complex (RISC)- mediates both cleavage and translational control (Mourelatos et al., 2002; Hutvágner and Zamore,

2002; Caudy et al., 2002; Martinez et al., 2002). Nonetheless, studies in both plants and animals show that at steady-state, siRNAs and miRNAs differ in at least one crucial respect: *in vivo* and *in vitro*, siRNAs are double-stranded, whereas miRNAs are single-stranded (Lee et al., 1993; Hamilton and Baulcombe, 1999; Pasquinelli et al., 2000; Reinhart et al., 2000; Elbashir et al., 2001a; Djikeng et al., 2001; Nykänen et al., 2001; Lagos-Quintana et al., 2001; Lau et al., 2001; Lee and Ambros, 2001; Lagos-Quintana et al., 2002; Reinhart et al., 2002; Llave et al., 2002a; Silhavy et al., 2002; Llave et al., 2002b; Tang et al., 2003).

siRNA duplexes can assemble into RISC in the absence of target mRNA, both in vivo and in vitro (Tuschl et al., 1999; Hammond et al., 2000; Zamore et al., 2000). Each RISC contains only one of the two strands of the siRNA duplex (Martinez et al., 2002). Since siRNA duplexes have no foreknowledge of which siRNA strand will guide target cleavage, both strands must assemble with the appropriate proteins to form a RISC. Previously, we and others showed that both siRNA strands are competent to direct RNAi (Tuschl et al., 1999; Hammond et al., 2000; Zamore et al., 2000; Elbashir et al., 2001b; Elbashir et al., 2001a; Nykänen et al., 2001). That is, the anti-sense strand of an siRNA can direct cleavage of a corresponding sense RNA target, whereas the sense siRNA strand directs cleavage of an anti-sense target. In this way, siRNA duplexes appear to be functionally symmetric. The ability to control which strand of an siRNA duplex enters into the RISC complex to direct cleavage of a corresponding RNA target would provide a significant advance for both research and therapeutic applications of RNAi technology.

Summary of the Invention

A key step in RNA interference (RNAi) is the assembly of a catalytically active protein-RNA complex, the RNA-induced silencing complex (RISC), that mediates target RNA cleavage. The instant invention is based, at least in part, on the discovery that the two strands of a siRNA duplex do not contribute equally to RISC assembly. Rather, both the absolute and the relative stabilites of the base pairs at the 5' ends of the two siRNA strands determines the degree to which each strand participates in the RNAi pathway. In fact, siRNA can be functionally asymmetric, with only one of the two strands able to trigger RNAi. The present invention is also based on the discovery that single stranded miRNAs are initially generated as siRNA-like duplexes whose structures predestine one

strand to enter the RISC and the other strand to be destroyed. This finding helps to explain the biogenesis of single-stranded miRNAs; the miRNA strand of a short-lived, siRNA duplex-like intermediate is assembled into a RISC complex, causing miRNAs to accumulate in vivo as single-stranded RNAs.

The present invention is further based on the discovery that RISC can cleave RNA targets with up to five contiguous mismatches at the siRNA 5′ end and eight mismatches at the siRNA 3′ end, indicating that 5′ bases contribute disproportionately to target RNA binding, but do not play a role in determining the catalytic rate, kcat. This finding explains how the 5′, central and 3′ sequences of the siRNA guide strand function to direct target cleavage.

The invention is further based on the discovery that the 3′ bases of the siRNA contribute much less than 5′ bases to the overall strength of binding, but instead help to establish the helical geometry required for RISC-mediated target cleavage, consistent with the view that catalysis by RISC requires a central A-form helix (Chiu et al., 2003). This finding indicates that complementarity is essential for translational repression by siRNAs designed to act like animal miRNAs, which typically repress translation (Doench et al., 2004).

The present invention is further based on the discovery that when an siRNA fails to pair with the first three, four or five nucleotides of the target RNA, the phosphodiester bond severed in the target RNA is unchanged; for perfectly matched siRNA, RISC measures the site of cleavage from the siRNA 5′ end (Elbashir et al., 2001; Elbashir et al., 2001). This finding indicates that the identity of the scissile phosphate is determined prior to the encounter of the RISC with its target RNA, perhaps because the RISC endonuclease is positioned with respect to the siRNA 5′ end during RISC assembly.

Accordingly, the instant invention features methods of enhancing the efficacy and specificity of RNAi. Also provided is a method of decreasing silencing of an inadvertent target by an RNAi agent. The invention further features compositions, including siRNAs, shRNAs, as well as vectors and transgenes, for mediating RNAi. The RNAi agents of the invention have improved specificity and efficacy in mediating silencing of a target gene.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

Brief Description of the Drawings

Figure 1. RNAi mediated by asymmetric duplex and single-stranded siRNAs. (A) Schematic showing relevant portions of the sense and anti-sense target RNA sequences. (B) Schematic showing siRNA duplex sequence and graph depicting RNAi mediated by the antisense and sense strands. (C) Schematic showing siRNA sequences of individual single strands and graph depicting RNAi mediated by the single strands. (D) Bar graph depicting fraction of total siRNA present as single-strand. (E) Schematic showing siRNA duplex sequence containing G:U wobble base pair and graph depicting RNAi mediated by the antisense and sense strands.

Figure 2. RNAi mediated by asymmetric duplex siRNAs. (A) Schematic showing relevant portions of the sense and anti-sense target RNA sequences. (B) Schematic showing siRNA duplex sequence and graph depicting RNAi mediated by the antisense and sense strands. (C) Schematic showing siRNA duplex sequence containing A:U mismatch and graph depicting RNAi mediated by the antisense and sense strands. (D) Schematic showing siRNA duplex sequence containing G:U mismatch and graph depicting RNAi mediated by the antisense and sense strands. (E) Schematic showing siRNA duplex sequence containing C:A mismatch and graph depicting RNAi mediated by the antisense and sense strands.

Figure 3. RNAi mediated by asymmetric duplex siRNAs. (A) Schematic showing relevant portions of the sense and anti-sense target RNA sequences. (B) Schematic showing siRNA duplex sequence and graph depicting RNAi mediated by the antisense and sense strands. (C) Schematic showing siRNA duplex sequence containing A:G mismatch and graph depicting RNAi mediated by the antisense and sense strands. (D) Schematic showing siRNA duplex sequence containing C:U mismatch and graph depicting RNAi mediated by the antisense and sense strands. (E) Schematic showing siRNA duplex sequence containing A:U base pair and graph depicting RNAi mediated by the antisense and sense strands. (F) Schematic showing siRNA duplex sequence containing A:G mismatch and graph depicting RNAi mediated by the antisense and sense strands. (G) Schematic showing siRNA duplex sequence containing C:U mismatch and graph depicting RNAi mediated by the antisense and sense strands. (H) Schematic showing siRNA duplex sequence containing A:U base pair and graph

depicting RNAi mediated by the antisense and sense strands. (I) Schematic of individual single-strands of siRNAs and graph depicting RNAi mediated by the individual single-strands.

Figure 4. RNAi mediated by asymmetric duplex siRNAs containing inosine. (A) Schematic showing siRNA duplex sequence having inosine at 5' end of sense strand and graph depicting RNAi mediated by the antisense and sense strands. (B) Schematic showing siRNA duplex sequence having inosine at 5' end of antisense strand and graph depicting RNAi mediated by the antisense and sense strands. (C) Schematic showing siRNA duplex sequence containing insoine in both strands and graph depicting RNAi mediated by the antisense and sense strands. (D) Schematic showing individual siRNA strands containing inosine and graph depicting RNAi mediated by the individual single-strands.

Figure 5. Symmetric cleavage of pre-*let-7* by Dicer. (A) Analysis of cleavage products produced on 5' side of precursor stem (*let-7*). (B) Analysis of cleavage products produced on 3' side of precursor stem (*let-7**). (C) Conceptual dicing of pre-*let-7* to a deduced pre-*let-7* siRNA.

Figure 6. Analysis of Drosphila miRNA genes for predicted miRNA and miRNA*. (A) Conceptual dicing of 26 published Drosphila miRNA genes to a deduced duplex siRNA. (B) Amounts of miR-10 and miR-10* detected *in vivo*.

Figure 7. Schematic representing mechanism of RISC assembly from pre-miRNA or dsRNA.

Figure 8. Reduction of off-target silencing by sense strand. (A) Sense and anti-sense *sod1* target RNA sequences. (B) Schematic showing siRNA duplex sequence and graph depicting RNAi mediated by the antisense and sense strands. (C) Schematic showing siRNA duplex sequence containing G:U wobble base pair and graph depicting RNAi mediated by the antisense and sense strands. (D) Schematic showing individual siRNA strands and graph depicting RNAi mediated by the individual single-strands. (E) Thermodynamic analysis of siRNA strand 5′ ends for the siRNA duplex in (B). ΔG (kcal/mole) was calculated in 1M NaCl at 37°C.

Figure 9. Enhancement of silencing by antisense strand. (A) Schematic showing relevant portions of the sense and anti-sense target RNA sequences. (B) Schematic showing siRNA duplex sequence and graph depicting RNAi mediated by the

antisense and sense strands. (B) Schematic showing siRNA duplex sequence containing A:U base pair and graph depicting RNAi mediated by the antisense and sense strands. (C) Schematic showing siRNA duplex sequence containing A:G mismatch and graph depicting RNAi mediated by the antisense and sense strands. (D) Thermodynamic analysis of siRNA strand 5′ends for the siRNA duplex in (B). ΔG (kcal/mole) was calculated in 1M NaCl at 37°C.

Figure 10. The relative thermodynamic stability of the first four base pairs of the siRNA strands explains siRNA functional asymmetry. Thermodynamic analysis of siRNA strand 5′ ends for the siRNAs in Figures 1B and 1E. ΔG (kcal/mole) was calculated in 1M NaCl at 37°C.

Figure 11. The first four base pairs of the siRNA duplex determine strand-specific activity. Internal, single-nucleotide mismatches (A-F) near the 5′ ends of an siRNA strand generate functional asymmetry, but internal G:U wobble pairs (G-I) do not.

Figure 12. Increased rate of siRNA efficiency when duplexes have dTdT mismatched tails.

Figure 13. Product release limits the rate of catalysis by RISC. (a) ATP stimulates multiple rounds of RISC cleavage of the RNA target. siRNA was incubated with ATP in Drosophila embryo lysate, then NEM was added to quench RISC assembly and to disable the ATP-regenerating system. The energy regenerating system was either restored by adding additional creatine kinase (+ATP) or the reaction was ATP-depleted by adding hexokinase and glucose (–ATP). The target RNA concentration was 49 nM and the concentration of RISC was ~4 nM. The siRNA sequence is given in Figure 21. (b) In the absence of ATP, cleavage by RISC produces a pre-steady state burst equal, within error, to the concentration of active RISC. The target concentration was 110 nM and the RISC concentration was ~4 nM. (c) Catalysis by RISC is not enhanced by ATP under single-turnover conditions. RISC was present in ~8-fold excess over target. Each data point represents the average of two trials.

Figure 14. In the absence of ATP, mismatches between the 3′ end of the siRNA guide strand and the target RNA facilitate product release, but reduce the rate of target cleavage. (a) Representative siRNA sequences are shown aligned with the target sequence. The siRNA guide strand is in color (5′ to 3′) and the mismatch with the target

site is highlighted in yellow. A complete list of siRNA sequences appears in Figure 21. (b) The steady-state rate of cleavage in the presence and absence of ATP was determined for siRNAs with zero to four 3′ mismatches with the target site. The target RNA concentration was 49 nM and the concentration of RISC was either ~4 nM (no mismatches) or ~6 nM (1 to 4 mismatches). The steady-state velocity with ATP, relative to the velocity without ATP is shown for each siRNA. (c) Time course of cleavage for perfectly matched (~16-fold excess of RISC relative to target) and mismatched (~80-fold excess of RISC) siRNA. (d) Data representative of those used in the analysis in (c) for target cleavage directed by siRNAs with zero, four, and five 3′ mismatches.

Figure 15. Remarkable tolerance of RISC for 3′ mismatches. (a) Each additional 3′ mismatch further reduced the rate of cleavage by RISC. The steady-state rates of cleavage were determined for siRNA with zero, one, two, and four mismatches under multiple-turnover conditions (~49 nM target mRNA and ~4–6 nM RISC). (b) Analysis of siRNAs bearing zero to five 3′ mismatches with the target RNA under conditions of slight enzyme excess (~2-fold more RISC than target). siRNA sequences used in (a) and (b) are shown in Figure 14A and Figure 21. (c) Extended endpoint analysis of RISC cleavage under conditions of ~80-fold enzyme excess reveals that cleavage can occur for siRNAs with as many as eight mismatches to the target RNA. Note the different time scales in (c) versus (b). All reactions were under standard in vitro RNAi (+ATP) conditions.

Figure 16. Limited tolerance of RISC for 5′ mismatches. (a) RISC cleavage was analyzed as in Figure 21C using 5′ mismatched siRNAs, whose sequences are given in Figure 21. The target RNA was the same for all siRNAs. (b) RISC cleavage was analyzed using a single siRNA sequence. Mismatches were created by altering the sequence of the target RNA. For the target containing compensatory mutations, the target concentration was 0.25 nM and the siRNA concentration was ~20 nM; RISC concentration was not determined. The asterisk denotes a 15 second time-point. (c) RISC cleavage was analyzed by incubating 50 nM siRNA with 0.5 nM target RNA. 3′ mismatches were created by modifying the target sequence, and 5′ mismatches by changing the siRNA. Target and siRNA sequences are given in Supplementary Figure 3. (d) Perfectly base-paired and 5′ mismatched siRNAs direct cleavage at the same phosphodiester bond. Cleavage reactions were performed with ~20 nM RISC generated from 50 nM siRNA and 0.5 nM target RNA and analyzed on an 8% denaturing

polyacrylamide sequencing gel. The target mRNA was 182 nt and 5′ cleavage product was 148 nt. After RISC was assembled, the extract was treated with NEM to inactivate nucleases (Schwartz et al., 2004). After NEM treatment, the ATP regenerating system was restored by adding additional creatine kinase, then target RNA was added and the incubation continued for the indicated time. OH– denotes a base hydrolysis ladder.

Figure 17. Michaelis-Menten and Ki analysis for matched and mismatched siRNAs reveal distinct contributions to binding and catalysis for the 5′, central, and 3′ regions of the siRNA. (a) siRNA was assembled into RISC under standard in vitro RNAi conditions, then diluted to achieve the desired RISC concentration. The initial rates of cleavage were determined for increasing concentrations of 5′ 32P-cap-radiolabled target mRNA. Plot of initial velocity versus substrate concentration. KM and Vmax were determined by fitting the data to the Michaelis-Menten equation. See Table 1 for analysis. Representative initial rate determinations appear in Figure 20A. (b) Ki values were determined in competition assays using 2′-O-methyl oligonucleotides bearing 5′, central, and 3′ mismatches to the siRNA guide strand. Representative data are presented in Figure 20B, and a complete list of the 2′-O-methyl oligonucleotides used appears in Figure 21.

Figure 18. A model for the cycle of RISC assembly, target recognition, catalysis, and recycling.

Figure 19. Exogenously programmed RISC is a bona fide enzyme siRNA was assembled into RISC for 1 hour in a standard in vitro RNAi reaction, then assembly was quenched with N-ethyl maleimide (NEM)21,29. The amount of RISC formed was determined by measuring 32P-radiolabeled siRNA retained on a tethered 5′-biotinylated, 31-nt, 2′-O-methyl oligonucleotide complementary to the guide strand of the siRNA. RISC binds essentially irreversibly to tethered 2′-O-methyl oligonucleotides, but cannot cleave these RNA-analogs (Hutvàgner et al., 2004; Schwartz et al., 2003). In all experiments, target-cleaving activity was not detected in the supernatant, demonstrating that all the active RISC was retained on the beads. (a) Sequence of the siRNA used (guide strand in red, 32P-radiolabel marked with an asterisk). Drosophila let-7 is not expressed in 0–2 hour embryos (Hutvàgner et al., 2001), so the only source of let-7 in the in vitro reactions was the exogenous let-7 siRNA. The 5′ end of the guide strand of the let-7 siRNA is predicted to be thermodynamically more stable than the 5′ end of the

passenger strand, explaining why only a low concentrations of let-7-programmed RISC is formed (Schwartz et al., 2003, Khvorova et al., 2003). The maximum amount of RISC assembled varies widely with siRNA sequence. The siRNAs used in Figures 3–8 were designed to load =5-fold more guide strand-containing RISC (Hutvàgner et al., 2001; Schwartz et al., 2003) (b) Representative gel confirming that the RISC was removed by the tethered 2′-O-methyl oligonucleotide. A reaction prior to incubation with the tethered 2′-O-methyl oligonucleotide (pre) was compared to the supernatant of a reaction incubated with beads alone (mock), and the supernatant of a reaction incubated with the complementary tethered 2′-O-methyl oligonucleotide (post). The buffer reaction contained no siRNA. (c) Analysis of the amount of RISC assembled at various siRNA concentrations. 5′ 32P-radiolabeled siRNA was incubated with lysate for 1 hour, then reactions were quenched by treatment with NEM, and RISC concentration was measured using the tethered 2′-O-methyl oligonucleotide method.

Figure 20. Michaelis-Menton and Competitor Analysis of RISC (a) Representative data for the determination of initial velocities for the perfectlymatched siRNA. Black, 1 nM target; red, 5 nM; blue, 20 nM; and green, 60 nM. (b) Three independent experiments for inhibition by a fully complementary 2′-O-methyl oligonucleotide competitor. ~1 nM RISC and 5 nM 32P-cap-radiolabeled target mRNA were incubated with increasing concentration of competitor, and the initial velocities were calculated and plotted versus competitor concentration.

Figure 21. siRNAs, target sites, and 2′-O-methyl oligonucleotides used in this study Table 1 Kinetic analysis of RISC.

Detailed Description of the Invention

A key step in RNA interference (RNAi) is the assembly of a catalytically active protein-RNA complex, the RNA-induced silencing complex (RISC), that mediates target RNA cleavage. Each RISC contains one of the two strands of the small interfering RNA (siRNA) duplex that triggers RNAi. The instant invention is based, at least in part, on the discovery that the two siRNA strands do not contribute equally to RISC assembly. Small changes in siRNA sequence were found to have profound and predictable effects on the extent to which the two strands of an siRNA duplex enter the RNAi pathway, a phenomenon termed siRNA functional "asymmetry". The discoveries described herein

reveal that the strength of the base-pairing interactions made by the 5′ end of each siRNA strand with the 3′ region of strand to which it is paired determines which of the two strands participates in the RNAi pathway. RISC assembly appears to be governed by an enzyme that initiates unwinding of an siRNA duplex at the siRNA strand whose 5′ end is less tightly paired to the complementary siRNA strand.

Remarkably, such highly asymmetric siRNA duplexes resemble proposed intermediates in the biogenesis pathway of microRNA (miRNA) (Hutvágner and Zamore, 2002; Reinhart et al., 2002; Lim et al., 2003b). miRNAs are endogenous, ~21-nt single-stranded RNAs processed by Dicer from stem-loop RNA precursors that regulate gene expression in animals and plants. A striking feature of miRNA precursors is their lack of full complementarity in the stem region. The discoveries presented herein indicate an important role for the discontinuities in the stem region of miRNAs; it is likely that miRNAs are initially generated from their precursor RNAs as siRNA-like duplexes, and that the structure of these duplexes predestines the miRNA strand to enter the RISC and the other strand to be destroyed. Thus, nature appears to have optimized the stem portion of miRNAs to follow a set of rules dictating which strand enters the RISC complex.

The discoveries made by the instant inventors provide rules according to which siRNAs and shRNAs can be designed that are fully asymmetric, with only one of the two siRNA strands competent to enter the RISC complex. By applying these rules to the selection and design of a targeted RNAi agent, e.g., siRNAs and shRNAs, the antisense strand of the RNAi agent can be predictably directed to enter the RISC complex and mediate target RNA cleavage. Similarly, the sense strand can be discouraged from entering the RISC complex, thereby reducing or eliminating undesired silencing of an inadvertent target by the sense strand.

Accordingly, the instant invention provides methods for improving the efficiency (or specificity) of an RNAi reaction comprising identifying an off target RNAi activity mediated by the sense strand of an RNAi agent, and modifying the RNAi agent such that the base pair strength between the 5' end of the antisense strand and the 3' end of the sense strand is lessened relative to the base pair strength of the 5' end of the sense strand and the 3' end of the antisense strand (*e.g.*, relative to the premodified RNAi agent),

such that the sense strand is less effective at entering RISC (*e.g.*, less effective than the premodified RNAi agent).

The instant invention also provides methods for improving the efficiency (or specificity) of an RNAi reaction comprising modifying (e.g., increasing) the asymmetry of the RNAi agent such that the ability of the sense or second strand to mediate RNAi (e.g., mediate cleavage of target RNA) is lessened. In preferred embodiments, the asymmetry is increased in favor of the 5' end of the first strand, e.g., lessening the bond strength (*e.g.*, the strength of the interaction) between the 5' end of the first strand and 3' end of the second strand relative to the bond strength (*e.g.*, the strength of the interaction) between the 5' end of the second strand and the 3' end of the first strand. . In other embodiments, the asymmetry is increased in favor of the 5' end of the first strand by increasing bond strength (*e.g.*, the strength of the interaction) between the 5' end of the second or sense strand and the 3' end of the first or antisense strand, relative to the bond strength (*e.g.*, the strength of the interaction) between the 5' end of the first and the 3' end of the second strand. In embodiments of the invention, the bond strength is increased, *e.g.*, the H bonding is increased between nucleotides or analogs at the 5' end, *e.g.*, within 5 nucleotides of the second or sense strand (numbered from the 5' end of the second strand) and complemtary nucleotides of the first or antisense strand. It is understood that the asymmetry can be zero (i.e., no asymmetry), for example, when the bonds or base pairs between the 5' and 3' terminal bases are of the same nature, strength or structure. More routinely, however, there exists some asymmetry due to the different nature, strength or structure of at least one nucleotide (often one or more nucleotides) between terminal nucleotides or nucleotide analogs.

Accordingly, in one aspect, the instant invention provides a method of enhancing the ability of a first strand of a RNAi agent to act as a guide strand in mediating RNAi, involving lessening the base pair strength between the 5' end of the first strand and the 3' end of a second strand of the duplex as compared to the base pair strength between the 3' end of the first strand and the 5' end of the second strand.

In a related aspect, the invention provides a method of enhancing the efficacy of a siRNA duplex, the siRNA duplex comprising a sense and an antisense strand, involving lessening the base pair strength between the antisense strand 5' end (AS 5') and the sense strand 3' end (S 3') as compared to the base pair strength between the

antisense strand 3' end (AS 3') and the sense strand 5' end (S '5), such that efficacy is enhanced.

In another aspect of the invention, a method is provided for promoting entry of a desired strand of an siRNA duplex into a RISC complex, comprising enhancing the asymmetry of the siRNA duplex, such that entry of the desired strand is promoted. In one embodiment of this aspect of the invention, the asymmetry is enhanced by lessening the base pair strength between the 5' end of the desired strand and the 3' end of a complementary strand of the duplex as compared to the base pair strength between the 3' end of the desired strand and the 5' end of the complementary strand.

In another aspect of the invention, a siRNA duplex is provided comprising a sense strand and an antisense strand, wherein the base pair strength between the antisense strand 5' end (AS 5') and the sense strand 3' end (S 3') is less than the base pair strength between the antisense strand 3' end (AS 3') and the sense strand 5' end (S '5), such that the antisense strand preferentially guides cleavage of a target mRNA.

In one embodiment of these aspects of the invention, the base-pair strength is less due to fewer G:C base pairs between the 5' end of the first or antisense strand and the 3' end of the second or sense strand than between the 3' end of the first or antisense strand and the 5' end of the second or sense strand.

In another embodiment, the base pair strength is less due to at least one mismatched base pair between the 5' end of the first or antisense strand and the 3' end of the second or sense strand. Preferably, the mismatched base pair is selected from the group consisting of G:A, C:A, C:U, G:G, A:A, C:C and U:U.

In one embodiment, the base pair strength is less due to at least one wobble base pair, e.g., G:U, between the 5' end of the first or antisense strand and the 3' end of the second or sense strand.

In another embodiment, the base pair strength is less due to at least one base pair comprising a rare nucleotide, e.g, inosine (I). Preferably, the base pair is selected from the group consisting of an I:A, I:U and I:C.

In yet another embodiment, the base pair strength is less due to at least one base pair comprising a modified nucleotide. In preferred embodiments, the modified nucleotide is selected from the group consisting of 2-amino-G, 2-amino-A, 2,6-diamino-G, and 2,6-diamino-A.

In several embodiments of these aspects of the invention, the RNAi agent is a siRNA duplex or is derived from an engineered precursor, and can be chemically synthesized or enzymatically synthesized.

In another aspect of the instant invention, compositions are provided comprising a siRNA duplex of the invention formulated to facilitate entry of the siRNA duplex into a cell. Also provided are pharmaceutical composition comprising a siRNA duplex of the invention.

Further provided are an engineered pre-miRNA comprising the siRNA duplex of any one of the preceding claims, as well as a vector encoding the pre-miRNA. In related aspects, the invention provides a pri-miRNA comprising the pre-miRNA, as well as a vector encoding the pri-miRNA.

Also featured in the instant invention are small hairpin RNA (shRNA) comprising nucleotide sequence identical to the sense and antisense strand of the siRNA duplex of any one of the preceding claims. In one embodiment, the nucleotide sequence identical to the sense strand is upstream of the nucleotide sequence identical to the antisense strand. In another embodiment, the nucleotide sequence identical to the antisense strand is upstream of the nucleotide sequence identical to the sense strand. Further provided are vectors and transgenes encoding the shRNAs of the invention.

In yet another aspect, the invention provides cells comprising the vectors featured in the instant invention. Preferably, the cell is a mammalian cell, e.g., a human cell.

In other aspects of the invention, methods of enhancing silencing of a target mRNA, comprising contacting a cell having an RNAi pathway with the RNAi agent of any one of the preceding claims under conditions such that silencing is enhanced.

Also provided are methods of enhancing silencing of a target mRNA in a subject, comprising administering to the subject a pharmaceutical composition comprising the RNAi agent of any one of the preceding claims such that silencing is enhanced.

Further provided is a method of decreasing silencing of an inadvertant target mRNA by a dsRNAi agent, the dsRNAi agent comprising a sense strand and an antisense strand involving the steps of: (a) detecting a significant degree of complementarity between the sense strand and the inadvertant target; and (b) enhancing the base pair strength between the 5' end of the sense strand and the 3' end of the antisense strand relative to the base pair strength between the 3' end of the sense strand

and the 5' end of the antisense strand; such that silencing of the inadvertant target mRNA is decreased. In a preferred embodiment, the silencing of the inadvertant target mRNA is decreased relative to silencing of a desired target mRNA

So that the invention may be more readily understood, certain terms are first defined.

The term "nucleoside" refers to a molecule having a purine or pyrimidine base covalently linked to a ribose or deoxyribose sugar. Exemplary nucleosides include adenosine, guanosine, cytidine, uridine and thymidine. The term "nucleotide" refers to a nucleoside having one or more phosphate groups joined in ester linkages to the sugar moiety. Exemplary nucleotides include nucleoside monophosphates, diphosphates and triphosphates. The terms "polynucleotide" and "nucleic acid molecule" are used interchangeably herein and refer to a polymer of nucleotides joined together by a phosphodiester linkage between 5' and 3' carbon atoms.

The term "RNA" or "RNA molecule" or "ribonucleic acid molecule" refers to a polymer of ribonucleotides. The term "DNA" or "DNA molecule" or deoxyribonucleic acid molecule" refers to a polymer of deoxyribonucleotides. DNA and RNA can be synthesized naturally (*e.g.*, by DNA replication or transcription of DNA, respectively). RNA can be post-transcriptionally modified. DNA and RNA can also be chemically synthesized. DNA and RNA can be single-stranded (*i.e.*, ssRNA and ssDNA, respectively) or multi-stranded (*e.g.*, double stranded, *i.e.*, dsRNA and dsDNA, respectively). "mRNA" or "messenger RNA" is single-stranded RNA that specifies the amino acid sequence of one or more polypeptide chains. This information is translated during protein synthesis when ribosomes bind to the mRNA.

As used herein, the term "small interfering RNA" ("siRNA") (also referred to in the art as "short interfering RNAs") refers to an RNA (or RNA analog) comprising between about 10-50 nucleotides (or nucleotide analogs) which is capable of directing or mediating RNA interference. Preferably, an siRNA comprises between about 15-30 nucleotides or nucleotide analogs, more preferably between about 16-25 nucleotides (or nucleotide analogs), even more preferably between about 18-23 nucleotides (or nucleotide analogs), and even more preferably between about 19-22 nucleotides (or nucleotide analogs) (*e.g.*, 19, 20, 21 or 22 nucleotides or nucleotide analogs).

As used herein, the term "rare nucleotide" refers to a naturally occurring nucleotide that occurs infrequently, including naturally occurring deoxyribonucleotides or ribonucleotides that occur infrequently, e.g., a naturally occurring ribonucleotide that is not guanosine, adenosine, cytosine, or uridine. Examples of rare nucleotides include, but are not limited to, inosine, 1-methyl inosine, pseudouridine, 5,6-dihydrouridine, ribothymidine, ^{2}N-methylguanosine and $^{2,2}N,N$-dimethylguanosine.

The term "nucleotide analog" or "altered nucleotide" or "modified nucleotide" refers to a non-standard nucleotide, including non-naturally occurring ribonucleotides or deoxyribonucleotides. Preferred nucleotide analogs are modified at any position so as to alter certain chemical properties of the nucleotide yet retain the ability of the nucleotide analog to perform its intended function. Examples of preferred modified nucleotides include, but are not limited to, 2-amino-guanosine, 2-amino-adenosine, 2,6-diamino-guanosine and 2,6-diamino-adenosine. Examples of positions of the nucleotide which may be derivitized include the 5 position, *e.g.*, 5-(2-amino)propyl uridine, 5-bromo uridine, 5-propyne uridine, 5-propenyl uridine, etc.; the 6 position, *e.g.*, 6-(2-amino)propyl uridine; the 8-position for adenosine and/or guanosines, *e.g.*, 8-bromo guanosine, 8-chloro guanosine, 8-fluoroguanosine, etc. Nucleotide analogs also include deaza nucleotides, *e.g.*, 7-deaza-adenosine; O- and N-modified (*e.g.*, alkylated, *e.g.*, N6-methyl adenosine, or as otherwise known in the art) nucleotides; and other heterocyclically modified nucleotide analogs such as those described in Herdewijn, *Antisense Nucleic Acid Drug Dev.*, 2000 Aug. 10(4):297-310.

Nucleotide analogs may also comprise modifications to the sugar portion of the nucleotides. For example the 2' OH-group may be replaced by a group selected from H, OR, R, F, Cl, Br, I, SH, SR, NH_2, NHR, NR_2, COOR, or OR, wherein R is substituted or unsubstituted C_1 –C_6 alkyl, alkenyl, alkynyl, aryl, etc. Other possible modifications include those described in U.S. Patent Nos. 5,858,988, and 6,291,438.

The phosphate group of the nucleotide may also be modified, *e.g.*, by substituting one or more of the oxygens of the phosphate group with sulfur (e.g., phosphorothioates), or by making other substitutions which allow the nucleotide to perform its intended function such as described in, for example, Eckstein, *Antisense Nucleic Acid Drug Dev.* 2000 Apr. 10(2):117-21, Rusckowski *et al. Antisense Nucleic Acid Drug Dev.* 2000 Oct. 10(5):333-45, Stein, *Antisense Nucleic Acid Drug Dev.* 2001

Oct. 11(5): 317-25, Vorobjev *et al. Antisense Nucleic Acid Drug Dev.* 2001 Apr. 11(2):77-85, and U.S. Patent No. 5,684,143. Certain of the above-referenced modifications (*e.g.*, phosphate group modifications) preferably decrease the rate of hydrolysis of, for example, polynucleotides comprising said analogs *in vivo* or *in vitro*.

The term "oligonucleotide" refers to a short polymer of nucleotides and/or nucleotide analogs. The term "RNA analog" refers to an polynucleotide (*e.g.*, a chemically synthesized polynucleotide) having at least one altered or modified nucleotide as compared to a corresponding unaltered or unmodified RNA but retaining the same or similar nature or function as the corresponding unaltered or unmodified RNA. As discussed above, the oligonucleotides may be linked with linkages which result in a lower rate of hydrolysis of the RNA analog as compared to an RNA molecule with phosphodiester linkages. For example, the nucleotides of the analog may comprise methylenediol, ethylene diol, oxymethylthio, oxyethylthio, oxycarbonyloxy, phosphorodiamidate, phophoroamidate, and/or phosphorothioate linkages. Preferred RNA analogues include sugar- and/or backbone-modified ribonucleotides and/or deoxyribonucleotides. Such alterations or modifications can further include addition of non-nucleotide material, such as to the end(s) of the RNA or internally (at one or more nucleotides of the RNA). An RNA analog need only be sufficiently similar to natural RNA that it has the ability to mediate (mediates) RNA interference.

As used herein, the term "RNA interference" ("RNAi") (also referred to in the art as "gene silencing" and/or "target silencing", *e.g.*, "target mRNA silencing") refers to a selective intracellular degradation of RNA. RNAi occurs in cells naturally to remove foreign RNAs (*e.g.*, viral RNAs). Natural RNAi proceeds *via* fragments cleaved from free dsRNA which direct the degradative mechanism to other similar RNA sequences. Alternatively, RNAi can be initiated by the hand of man, for example, to silence the expression of target genes.

As used herein, the term "antisense strand" of an siRNA or RNAi agent refers to a strand that is substantially complementary to a section of about 10-50 nucleotides, e.g., about 15-30, 16-25, 18-23 or 19-22 nucleotides of the mRNA of the gene targeted for silencing. The antisense strand or first strand has sequence sufficiently complementary to the desired target mRNA sequence to direct target-specific RNA interference (RNAi), e.g., complementarity sufficient to trigger the destruction of the desired target mRNA by

the RNAi machinery or process. The term "sense strand" or "second strand" of an siRNA or RNAi agent refers to a strand that is complementary to the antisense strand or first strand. Antisense and ssense strands can also be referred to as first or second strands, the first or second strand having complementarity to the target sequence and the respective second or first strand having complementarity to said first or second strand.

As used herein, the term "guide strand" refers to a strand of an RNAi agent, e.g., an antisense strand of an siRNA duplex, that enters into the RISC complex and directs cleavage of the target mRNA.

A "target gene" is a gene whose expression is to be selectively inhibited or "silenced." This silencing is achieved by cleaving the mRNA of the target gene by an siRNA or miRNA, *e.g.*, an siRNA or miRNA that is created from an engineered RNA precursor by a cell's RNAi system. One portion or segment of a duplex stem of the RNA precursor is an anti-sense strand that is complementary, e.g., sufficiently complementary to trigger the destruction of the desired target mRNA by the RNAi machinery or process, to a section of about 18 to about 40 or more nucleotides of the mRNA of the target gene.

The term "engineered," as in an engineered RNA precursor, or an engineered nucleic acid molecule, indicates that the precursor or molecule is not found in nature, in that all or a portion of the nucleic acid sequence of the precursor or molecule is created or selected by man. Once created or selected, the sequence can be replicated, translated, transcribed, or otherwise processed by mechanisms within a cell. Thus, an RNA precursor produced within a cell from a transgene that includes an engineered nucleic acid molecule is an engineered RNA precursor.

As used herein, the term "asymmetry", as in the asymmetry of a siRNA duplex, refers to an inequality of bond strength or base pairing strength between the siRNA termini (e.g., between terminal nucleotides on a first strand and terminal nucleotides on an opposing second strand), such that the 5' end of one strand of the duplex is more frequently in a transient unpaired, *e.g*, single-stranded, state than the 5' end of the complementary strand. This structural difference determines that one strand of the duplex is preferentially incorporated into a RISC complex. The strand whose 5' end is less tightly paired to the complementary strand will preferentially be incorporated into RISC and mediate RNAi.

As used herein, the term "bond strength" or "base pair strength" refers to the strength of the interaction between pairs of nucleotides (or nucleotide analogs) on opposing strands of an oligonucleotide duplex (e.g., an siRNA duplex), due primarily to H-bonding, Van der Waals interactions, and the like between said nucleotides (or nucleotide analogs).

As used herein, the "5' end", as in the 5' end of an antisense strand, refers to the 5' terminal nucleotides, e.g., between one and about 5 nucleotides at the 5' terminus of the antisense strand. As used herein, the "3' end", as in the 3' end of a sense strand, refers to the region, *e.g.*, a region of between one and about 5 nucleotides, that is complementary to the nucleotides of the 5' end of the complementary antisense strand.

As used herein, the term "isolated RNA" (*e.g.*, "isolated shRNA", "isolated siRNA" or "isolated RNAi agent") refers to RNA molecules which are substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

As used herein, the term "transgene" refers to any nucleic acid molecule, which is inserted by artifice into a cell, and becomes part of the genome of the organism that develops from the cell. Such a transgene may include a gene that is partly or entirely heterologous (i.e., foreign) to the transgenic organism, or may represent a gene homologous to an endogenous gene of the organism. The term "transgene" also means a nucleic acid molecule that includes one or more selected nucleic acid sequences, e.g., DNAs, that encode one or more engineered RNA precursors, to be expressed in a transgenic organism, e.g., animal, which is partly or entirely heterologous, i.e., foreign, to the transgenic animal, or homologous to an endogenous gene of the transgenic animal, but which is designed to be inserted into the animal's genome at a location which differs from that of the natural gene. A transgene includes one or more promoters and any other DNA, such as introns, necessary for expression of the selected micleic acid sequence, all operably linked to the selected sequence, and may include an enhancer sequence.

The term "*in vitro*" has its art recognized meaning, *e.g.*, involving purified reagents or extracts, *e.g.*, cell extracts. The term "*in vivo*" alos has its art recognized meaning, *e.g.*, involving living cells, *e.g.*, immortalized cells, primary cells, cell lines, and/or cells in an organism.

A gene "involved" in a disorder includes a gene, the normal or aberrant expression or function of which effects or causes a disease or disorder or at least one symptom of said disease or disorder

Various methodologies of the instant invention include step that involves comparing a value, level, feature, characteristic, property, etc. to a "suitable control", referred to interchangeably herein as an "appropriate control". A "suitable control" or "appropriate control" is any control or standard familiar to one of ordinary skill in the art useful for comparison purposes. In one embodiment, a "suitable control" or "appropriate control" is a value, level, feature, characteristic, property, etc. determined prior to performing an RNAi methodology, as described herein. For example, a transcription rate, mRNA level, translation rate, protein level, biological activity, cellular characteristic or property, genotype, phenotype, etc. can be determined prior to introducing an RNAi agent of the invention into a cell or organism. In another embodiment, a "suitable control" or "appropriate control" is a value, level, feature, characteristic, property, etc. determined in a cell or organism, *e.g.*, a control or normal cell or organism, exhibiting, for example, normal traits. In yet another embodiment, a "suitable control" or "appropriate control" is a predefined value, level, feature, characteristic, property, etc.

Various aspects of the invention are described in further detail in the following subsections.

I. RNA molecules and agents

The present invention features "small interfering RNA molecules" ("siRNA molecules" or "siRNA"), methods of making said siRNA molecules and methods (*e.g.*, research and/or therapeutic methods) for using said siRNA molecules. An siRNA molecule of the invention is a duplex consisting of a sense strand and complementary antisense strand, the antisense strand having sufficient complementarity to a target mRNA to mediate RNAi. Preferably, the strands are aligned such that there are at least 1, 2, or 3 bases at the end of the strands which do not align (*i.e.*, for which no complementary bases occur in the opposing strand) such that an overhang of 1, 2 or 3 residues occurs at one or both ends of the duplex when strands are annealed. Preferably,

the siRNA molecule has a length from about 10-50 or more nucleotides, *i.e.*, each strand comprises 10-50 nucleotides (or nucleotide analogs). More preferably, the siRNA molecule has a length from about 15-45 or 15-30 nucleotides. Even more preferably, the siRNA molecule has a length from about 16-25 or 18-23 nucleotides. The siRNA molecules of the invention further have a sequence that is "sufficiently complementary" to a target mRNA sequence to direct target-specific RNA interference (RNAi), as defined herein, *i.e.*, the siRNA has a sequence sufficient to trigger the destruction of the target mRNA by the RNAi machinery or process.

siRNAs featured in the invention provide enhanced specificity and efficacy for mediating RISC-mediated cleavage of a desired target gene. In preferred aspect, the base pair strength between the antisense strand 5' end (AS 5') and the sense strand 3' end (S 3') of the siRNAs is less than the bond strength or base pair strength between the antisense strand 3' end (AS 3') and the sense strand 5' end (S '5), such that the antisense strand preferentially guides cleavage of a target mRNA. In one embodiment, the bond strength or base-pair strength is less due to fewer G:C base pairs between the 5' end of the first or antisense strand and the 3' end of the second or sense strand than between the 3' end of the first or antisense strand and the 5' end of the second or sense strand.

In another embodiment, the bond strength or base pair strength is less due to at least one mismatched base pair between the 5' end of the first or antisense strand and the 3' end of the second or sense strand. Preferably, the mismatched base pair is selected from the group consisting of G:A, C:A, C:U, G:G, A:A, C:C and U:U. In a related embodiment, the bond strength or base pair strength is less due to at least one wobble base pair, e.g., G:U, between the 5' end of the first or antisense strand and the 3' end of the second or sense strand.

In yet another embodiment, the bond strength or base pair strength is less due to at least one base pair comprising a rare nucleotide, e.g, inosine (I). Preferably, the base pair is selected from the group consisting of an I:A, I:U and I:C.

In yet another embodiment, the bond strength or base pair strength is less due to at least one base pair comprising a modified nucleotide. In preferred embodiments, the modified nucleotide is selected from the group consisting of 2-amino-G, 2-amino-A, 2,6-diamino-G, and 2,6-diamino-A.

In general, siRNA containing nucleotide sequences sufficiently identical to a portion of the target gene to effect RISC-mediated cleavage of the target gene are preferred. 100% sequence identity between the siRNA and the target gene is not required to practice the present invention. The invention has the advantage of being able to tolerate preferred sequence variations of the methods and compositions of the invention in order to enhance efficiency and specificity of RNAi. For example, siRNA sequences with insertions, deletions, and single point mutations relative to the target sequence can also be effective for inhibition. Alternatively, siRNA sequences with nucleotide analog substitutions or insertions can be effective for inhibition

Sequence identity may determined by sequence comparison and alignment algorithms known in the art. To determine the percent identity of two nucleic acid sequences (or of two amino acid sequences), the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the first sequence or second sequence for optimal alignment). The nucleotides (or amino acid residues) at corresponding nucleotide (or amino acid) positions are then compared. When a position in the first sequence is occupied by the same residue as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100), optionally penalizing the score for the number of gaps introduced and/or length of gaps introduced.

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In one embodiment, the alignment generated over a certain portion of the sequence aligned having sufficient identity but not over portions having low degree of identity (*i.e.*, a local alignment). A preferred, non-limiting example of a local alignment algorithm utilized for the comparison of sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-77. Such an algorithm is incorporated into the BLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10.

In another embodiment, the alignment is optimized by introducing appropriate gaps and percent identity is determined over the length of the aligned sequences (*i.e.*, a gapped alignment). To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. In another embodiment, the alignment is optimized by introducing appropriate gaps and percent identity is determined over the entire length of the sequences aligned (*i.e.*, a global alignment). A preferred, non-limiting example of a mathematical algorithm utilized for the global comparison of sequences is the algorithm of Myers and Miller, *CABIOS* (1989). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

Greater than 80% sequence identity, *e.g.*, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or even 100% sequence identity, between the siRNA antisense strand and the portion of the target gene is preferred. Alternatively, the siRNA may be defined functionally as a nucleotide sequence (or oligonucleotide sequence) that is capable of hybridizing with a portion of the target gene transcript (e.g., 400 mM NaCl, 40 mM PIPES pH 6.4, 1 mM EDTA, 50°C or 70°C hybridization for 12-16 hours; followed by washing). Additional preferred hybridization conditions include hybridization at 70°C in 1xSSC or 50°C in 1xSSC, 50% formamide followed by washing at 70°C in 0.3xSSC or hybridization at 70°C in 4xSSC or 50°C in 4xSSC, 50% formamide followed by washing at 67°C in 1xSSC. The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (Tm) of the hybrid, where Tm is determined according to the following equations. For hybrids less than 18 base pairs in length, Tm(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, Tm(°C) = 81.5 + 16.6(log10[Na+]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na+] is the concentration of sodium ions in the hybridization buffer ([Na+] for 1xSSC = 0.165 M). Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY,

chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference. The length of the identical nucleotide sequences may be at least about 10, 12, 15, 17, 20, 22, 25, 27, 30, 32, 35, 37, 40, 42, 45, 47 or 50 bases.

The RNA molecules of the present invention can be modified to improve stability in serum or in growth medium for cell cultures. In order to enhance the stability, the 3'-residues may be stabilized against degradation, *e.g.*, they may be selected such that they consist of purine nucleotides, particularly adenosine or guanosine nucleotides. Alternatively, substitution of pyrimidine nucleotides by modified analogues, *e.g.*, substitution of uridine by 2'-deoxythymidine is tolerated and does not affect the efficiency of RNA interference.

In a preferred aspect, the invention features small interfering RNAs (siRNAs) that include a sense strand and an antisense strand, wherein the antisense strand has a sequence sufficiently complementary to a target mRNA sequence to direct target-specific RNA interference (RNAi) and wherein the sense strand and/or antisense strand is modified by the substitution of internal nucleotides with modified nucleotides, such that *in vivo* stability is enhanced as compared to a corresponding unmodified siRNA. As defined herein, an "internal" nucleotide is one occurring at any position other than the 5' end or 3' end of nucleic acid molecule, polynucleotide or oligonucleoitde. An internal nucleotide can be within a single-stranded molecule or within a strand of a duplex or double-stranded molecule. In one embodiment, the sense strand and/or antisense strand is modified by the substitution of at least one internal nucleotide. In another embodiment, the sense strand and/or antisense strand is modified by the substitution of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more internal nucleotides. In another embodiment, the sense strand and/or antisense strand is modified by the substitution of at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more of the internal nucleotides. In yet another embodiment, the sense strand and/or antisense strand is modified by the substitution of all of the internal nucleotides.

In a preferred embodiment of the present invention the RNA molecule may contain at least one modified nucleotide analogue. The nucleotide analogues may be located at positions where the target-specific activity, *e.g.*, the RNAi mediating activity is not substantially effected, *e.g.*, in a region at the 5'-end and/or the 3'-end of the RNA

molecule. Particularly, the ends may be stabilized by incorporating modified nucleotide analogues.

Preferred nucleotide analogues include sugar- and/or backbone-modified ribonucleotides (*i.e.*, include modifications to the phosphate-sugar backbone). For example, the phosphodiester linkages of natural RNA may be modified to include at least one of a nitrogen or sulfur heteroatom. In preferred backbone-modified ribonucleotides the phosphoester group connecting to adjacent ribonucleotides is replaced by a modified group, *e.g.*, of phosphothioate group. In preferred sugar-modified ribonucleotides, the 2' OH-group is replaced by a group selected from H, OR, R, halo, SH, SR, NH_2, NHR, NR_2 or ON, wherein R is C_1-C_6 alkyl, alkenyl or alkynyl and halo is F, Cl, Br or I.

Also preferred are nucleobase-modified ribonucleotides, *i.e.*, ribonucleotides, containing at least one non-naturally occurring nucleobase instead of a naturally occurring nucleobase. Bases may be modified to block the activity of adenosine deaminase. Exemplary modified nucleobases include, but are not limited to, uridine and/or cytidine modified at the 5-position, *e.g.*, 5-(2-amino)propyl uridine, 5-bromo uridine; adenosine and/or guanosines modified at the 8 position, *e.g.*, 8-bromo guanosine; deaza nucleotides, *e.g.*, 7-deaza-adenosine; O- and N-alkylated nucleotides, *e.g.*, N6-methyl adenosine are suitable. It should be noted that the above modifications may be combined.

RNA may be produced enzymatically or by partial/total organic synthesis, any modified nibonucleotide can be introduced by *in vitro* enzymatic or organic synthesis. In one embodiment, an RNAi agent is prepared chemically. Methods of synthesizing RNA molecules are known in the art, in particular, the chemical synthesis methods as de scribed in Verma and Eckstein (1998) *Annul Rev. Biochem.* 67:99-134. In another embodiment, a ss-siRNA is prepared enzymatically. For example, a ds-siRNA can be prepared by enzymatic processing of a long ds RNA having sufficient complementarity to the desired target mRNA. Processing of long ds RNA can be accomplished *in vitro*, for example, using appropriate cellular lysates and ds-siRNAs can be subsequently purified by gel electrophoresis or gel filtration. ds-siRNA can then be denatured according to art-recognized methodologies. In an exemplary embodiment, RNA can be purified from a mixture by extraction with a solvent or resin, precipitation,

electrophoresis, chromatography, or a combination thereof. Alternatively, the RNA may be used with no or a minimum of purification to avoid losses due to sample processing. Alternatively, the siRNA can also be prepared by enzymatic transcription from synthetic DNA templates or from DNA plasmids isolated from recombinant bacteria. Typically, phage RNA polymerases are used such as T7, T3 or SP6 RNA polymerase (Milligan and Uhlenbeck (1989) *Methods Enzymol.* 180:51-62). The RNA may be dried for storage or dissolved in an aqueous solution. The solution may contain buffers or salts to inhibit annealing, and/or promote stabilization of the single strands.

In one embodiment, the target mRNA of the invention specifies the amino acid sequence of a cellular protein (*e.g.*, a nuclear, cytoplasmic, transmembrane, or membrane-associated protein). In another embodiment, the target mRNA of the invention specifies the amino acid sequence of an extracellular protein (*e.g.*, an extracellular matrix protein or secreted protein). As used herein, the phrase "specifies the amino acid sequence" of a protein means that the mRNA sequence is translated into the amino acid sequence according to the rules of the genetic code. The following classes of proteins are listed for illustrative purposes: developmental proteins (*e.g.*, adhesion molecules, cyclin kinase inhibitors, Wnt family members, Pax family members, Winged helix family members, Hox family members, cytokines/lymphokines and their receptors, growth/differentiation factors and their receptors, neurotransmitters and their receptors); oncogene-encoded proteins (*e.g.*, ABLI, BCLI, BCL2, BCL6, CBFA2, CBL, CSFIR, ERBA, ERBB, EBRB2, ETSI, ETSI, ETV6, FGR, FOS, FYN, HCR, HRAS, JUN, KRAS, LCK, LYN, MDM2, MLL, MYB, MYC, MYCLI, MYCN, NRAS, PIM I, PML, RET, SRC, TALI, TCL3, and YES); tumor suppressor proteins (*e.g.*, APC, BRCA1, BRCA2, MADH4, MCC, NF I, NF2, RB I, TP53, and WTI); and enzymes (*e.g.*, ACC synthases and oxidases, ACP desaturases and hydroxylases, ADP-glucose pyrophorylases, ATPases, alcohol dehydrogenases, amylases, amyloglucosidases, catalases, cellulases, chalcone synthases, chitinases, cyclooxygenases, decarboxylases, dextriinases, DNA and RNA polymerases, galactosidases, glucanases, glucose oxidases, granule-bound starch synthases, GTPases, helicases, hernicellulases, integrases, inulinases, invertases, isomerases, kinases, lactases, lipases, lipoxygenases, lysozymes, nopaline synthases, octopine synthases, pectinesterases, peroxidases, phosphatases, phospholipases, phosphorylases, phytases, plant growth regulator synthases, polygalacturonases, proteinases and peptidases,

pullanases, recombinases, reverse transcriptases, RUBISCOs, topoisomerases, and xylanases).

In a preferred aspect of the invention, the target mRNA molecule of the invention specifies the amino acid sequence of a protein associated with a pathological condition. For example, the protein may be a pathogen-associated protein (*e.g.*, a viral protein involved in immunosuppression of the host, replication of the pathogen, transmission of the pathogen, or maintenance of the infection), or a host protein which facilitates entry of the pathogen into the host, drug metabolism by the pathogen or host, replication or integration of the pathogen's genome, establishment or spread of infection in the host, or assembly of the next generation of pathogen. Alternatively, the protein may be a tumor-associated protein or an autoimmune disease-associated protein.

In one embodiment, the target mRNA molecule of the invention specifies the amino acid sequence of an endogenous protein (*i.e.*, a protein present in the genome of a cell or organism). In another embodiment, the target mRNA molecule of the invention specified the amino acid sequence of a heterologous protein expressed in a recombinant cell or a genetically altered organism. In another embodiment, the target mRNA molecule of the invention specified the amino acid sequence of a protein encoded by a transgene (*i.e.*, a gene construct inserted at an ectopic site in the genome of the cell). In yet another embodiment, the target mRNA molecule of the invention specifies the amino acid sequence of a protein encoded by a pathogen genome which is capable of infecting a cell or an organism from which the cell is derived.

By inhibiting the expression of such proteins, valuable information regarding the function of said proteins and therapeutic benefits which may be obtained from said inhibition may be obtained.

In one embodiment, siRNAs are synthesized either *in vivo*, *in situ*, or *in vitro*. Endogenous RNA polymerase of the cell may mediate transcription *in vivo* or *in situ*, or cloned RNA polymerase can be used for transcription *in vivo* or *in vitro*. For transcription from a transgene *in vivo* or an expression construct, a regulatory region (*e.g.*, promoter, enhancer, silencer, splice donor and acceptor, polyadenylation) may be used to transcribe the ss-siRNA. Inhibition may be targeted by specific transcription in an organ, tissue, or cell type; stimulation of an environmental condition (*e.g.*, infection, stress, temperature, chemical inducers); and/or engineering transcription at a

developmental stage or age. A transgenic organism that expresses ss-siRNA from a recombinant construct may be produced by introducing the construct into a zygote, an embryonic stem cell, or another multipotent cell derived from the appropriate organism.

II. Short hairpin RNAs (shRNAs)

In certain featured embodiments, the instant invention provides shRNAs having enhanced specificity or efficacy in mediating RNAi. In contrast to short siRNA duplexes, short hairpin RNAs (shRNAs) mimic the natural precursors of miRNAs and enter at the top of the RNAi pathway. For this reason, shRNAs are believed to mediate RNAi more efficiently by being fed through the entire natural RNAi pathway.

A preferred shRNA of the invention is one that has been redesigned for increased specificity or enhancement relative to a previous shRNA. The new shRNA differs from a previous shRNA in that an siRNA duplex produced from the new shRNA has less base pair strength between the 5' end of the antisense strand or first strand and the 3' end of the sense strand or second strand than the base pair strength between the 3' end of the antisense strand or first strand and the 5' end of the sense strand or second strand.

1. Engineered RNA Precursors That Generate siRNAs

Naturally-occurring miRNA precursors (pre-miRNA) have a single strand that forms a duplex stem including two portions that are generally complementary, and a loop, that connects the two portions of the stem. In typical pre-miRNAs, the stem includes one or more bulges, e.g., extra nucleotides that create a single nucleotide "loop" in one portion of the stem, and/or one or more unpaired nucleotides that create a gap in the hybridization of the two portions of the stem to each other. Short hairpin RNAs, or engineered RNA precursors, of the invention are artificial constructs based on these naturally occurring pre-miRNAs, but which are engineered to deliver desired siRNAs.

In shRNAs, or engineered precursor RNAs, of the instant invention, one portion of the duplex stem is a nucleic acid sequence that is complementary (or anti-sense) to the target mRNA. Thus, engineered RNA precursors include a duplex stem with two portions and a loop connecting the two stem portions. The two stem portions are about 18 or 19 to about 25, 30, 35, 37, 38, 39, or 40 or more nucleotides in length. When used

in mammalian cells, the length of the stem portions should be less than about 30 nucleotides to avoid provoking non-specific responses like the interferon pathway. In non-mammalian cells, the stem can be longer than 30 nucleotides. In fact, the stem can include much larger sections complementary to the target mRNA (up to, and including the entire mRNA). The two portions of the duplex stem must be sufficiently complementary to hybridize to form the duplex stem. Thus, the two portions can be, but need not be, fully or perfectly complementary. In addition, the two stem portions can be the same length, or one portion can include an overhang of 1, 2, 3, or 4 micleotides. The overhanging nucleotides can include, for example, uracils (Us), e.g., all Us. The loop in the shRNAs or engineered RNA precursors may differ from natural pre-miRNA sequences by modifying the loop sequence to increase or decrease the number of paired nucleotides, or replacing all or part of the loop sequence with a tetraloop or other loop sequences. Thus, the loop in the shRNAs or engineered RNA precursors can be 2, 3, 4, 5, 6, 7, 8, 9, or more, *e.g.*, 15 or 20, or more nucleotides in length.

shRNAs of the invention include the sequences of the desired siRNA duplex. The desired siRNA duplex, and thus both of the two stem portions in the engineered RNA precursor, are selected by methods known in the art. These include, but are not limited to, selecting an 18, 19, 20, 21 nucleotide, or longer, sequence from the target gene mRNA sequence from a region 100 to 200 or 300 nucleotides on the 3' side of the start of translation. In general, the sequence can be selected from any portion of the mRNA from the target gene, such as the 5' UTR (untranslated region), coding sequence, or 3' UTR. This sequence can optionally follow immediately after a region of the target gene containing two adjacent AA nucleotides. The last two nucleotides of the 21 or so nucleotide sequence can be selected to be UU (so that the anti-sense strand of the siRNA begins with UU). This 21 or so nucleotide sequence is used to create one portion of a duplex stem in the engineered RNA precursor. This sequence can replace a stem portion of a wild-type pre-stRNA sequence, e.g., enzymatically, or is included in a complete sequence that is synthesized. For example, one can synthesize DNA oligonucleotides that encode the entire stem-loop engineered RNA precursor, or that encode just the portion to be inserted into the duplex stem of the precursor, and using restriction enzymes to build the engineered RNA precursor construct, *e.g.*, from a wild-type pre-stRNA.

Engineered RNA precursors include in the duplex stem the 21-22 or so nucleotide sequences of the siRNA desired to be produced *in vivo*. Thus, the stem portion of the engineered RNA precursor includes at least 18 or 19 nucleotide pairs corresponding to the sequence of an exonic portion of the gene whose expression is to be reduced or inhibited. The two 3' nucleotides flanking this region of the stem are chosen so as to maximize the production of the siRNA from the engineered RNA precursor, and to maximize the efficacy of the resulting siRNA in targeting the corresponding mRNA for destruction by RNAi *in vivo* and *in vitro*.

Another defining feature of these engineered RNA precursors is that as a consequence of their length, sequence, and/or structure, they do not induce sequence non-specific responses, such as induction of the interferon response or apoptosis, or that they induce a lower level of such sequence non-specific responses than long, double-stranded RNA (>150bp) that has been used to induce RNAi. For example,the interferon response is triggered by dsRNA longer than 30 base pairs.

2. Transgenes Encoding Engineered RNA Precursors

The new engineered RNA precursors can be synthesized by standard methods known in the art, *e.g.*, by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). These synthetic, engineered RNA precursors can be used directly as described below or cloned into expression vectors by methods known in the field. The engineered RNA precursors should be delivered to cells *in vitro* or *in vivo* in which it is desired to target a specific mRNA for destruction. A number of methods have been developed for delivering DNA or RNA to cells. For example, for in vivo delivery, molecules can be injected directly into a tissue site or administered systemically. *In vitro* delivery includes methods known in the art such as electroporation and lipofection.

To achieve intracellular concentrations of the nucleic acid molecule sufficient to suppress expression of endogenous mRNAs, one can use, for example, a recombinant DNA construct in which the oligonucleotide is placed under the control of a strong *Pol* III (e.g., U6 or *Pol*III H1-RNA promoter) or *Pol* II promoter. The use of such a construct to transfect target cells *in vitro* or *in vivo* will result in the transcription of sufficient amounts of the engineered RNA precursor to lead to the production of an siRNA that

can target a corresponding mRNA sequence for cleavage by RNAi to decrease the expression of the gene encoding that mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an engineered RNA precursor. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired stRNA precursor.

Such vectors can be constructed by recombinant DNA technology methods known in the art. Vectors can be plasmid, viral, or other vectors known in the art such as those described herein, used for replication and expression in mammalian cells or other targeted cell types. The nucleic acid sequences encoding the engineered RNA precursors can be prepared using known techniques. For example, two synthetic DNA oligonucleotides can be synthesized to create a novel gene encoding the entire engineered RNA precursor. The DNA oligonucleotides, which will pair, leaving appropriate 'sticky ends' for cloning, can be inserted into a restriction site in a plasmid that contains a promoter sequence (e.g., a *Pol* II or a *Pol* III promoter) and appropri ate terminator sequences 3' to the enginered RNA precursor sequences (*e.g.*, a cleavage and polyadenylation signal sequence from SV40 or a *Pol* III terminator sequence).

The invention also encompasses genetically engineered host cells that contain any of the foregoing expression vectors and thereby express the nucleic acid molecules of the invention in the host cell. The host cells can be cultured using known techniques and methods (see, *e.g.*, Culture of Animal Cells (R.I. Freshney, Alan R. Liss, Inc. 1987); Molecular Cloning, Sambrook et al. (Cold Spring Harbor Laboratory Press, 1989)).

Successful introduction of the vectors of the invention into host cells can be monitored using various known methods. For example, transient transfection can be signaled with a reporter, such as a fluorescent marker, such as Green Fluorescent Protein (GFP). Stable transfection can be indicated using markers that provide the transfected cell with resistance to specific environmental factors (*e.g.*, antibiotics and drugs), such as hygromycin B resistance, *e.g.*, in insect cells and in mammalian cells.

3. Regulatory Sequences

The expression of the engineered RNA precursors is driven by regulatory sequences, and the vectors of the invention can include any regulatory sequences known in the art to act in mammalian cells, *e.g.*, human or murine cells; in insect cells; in plant

cells; or other cells. The term regulatory sequence includes promoters, enhancers, and other expression control elements. It will be appreciated that the appropriate regulatory sequence depends on such factors as the future use of the cell or transgenic animal into which a sequence encoding an engineered RNA precursor is being introduced, and the level of expression of the desired RNA precursor. A person skilled in the art would be able to choose the appropriate regulatory sequence. For example, the transgenic animals described herein can be used to determine the role of a test polypeptide or the engineered RNA precursors in a particular cell type, *e.g.*, a hematopoietic cell. In this case, a regulatory sequence that drives expression of the transgene ubiquitously, or a hematopoietic-specific regulatory sequence that expresses the transgene only in hematopoietic cells, can be used. Expression of the engineered RNA precursors in a hematopoietic cell means that the cell is now susceptible to specific, targeted RNAi of a particular gene. Examples of various regulatory sequences are described below.

The regulatory sequences can be inducible or constitutive. Suitable constitutive regulatory sequences include the regulatory sequence of a housekeeping gene such as the α-actin regulatory sequence, or may be of viral origin such as regulatory sequences derived from mouse mammary tumor virus (MMTV) or cytomegalovirus (CMV).

Alternatively, the regulatory sequence can direct transgene expression in specific organs or cell types (see, *e.g.*, Lasko et al., 1992, *Proc. Natl. Acad. Sci.* USA 89:6232). Several tissue-specific regulatory sequences are known in the art including the albumin regulatory sequence for liver (Pinkert et al., 1987, *Genes Dev.* 1:268276); the endothelin regulatory sequence for endothelial cells (Lee, 1990, *J. Biol. Chem.* 265:10446-50); the keratin regulatory sequence for epidermis; the myosin light chain-2 regulatory sequence for heart (Lee et al., 1992, *J. Biol. Chem.* 267:15875-85), and the insulin regulatory sequence for pancreas (Bucchini et al., 1986, *Proc. Natl. Acad. Sci.* USA 83:2511-2515), or the vav regulatory sequence for hematopoietic cells (Oligvy et al., 1999, *Proc. Natl. Acad. Sci.* USA 96:14943-14948). Another suitable regulatory sequence, which directs constitutive expression of transgenes in cells of hematopoietic origin, is the murine MHC class I regulatory sequence (Morello et al., 1986, *EMBO J.* 5:1877-1882). Since NMC expression is induced by cytokines, expression of a test gene operably linked to this regulatory sequence can be upregulated in the presence of cytokines.

In addition, expression of the transgene can be precisely regulated, for example, by using an inducible regulatory sequence and expression systems such as a regulatory sequence that is sensitive to certain physiological regulators, *e.g.*, circulating glucose levels, or hormones (Docherty et al., 1994, FASEB J. 8:20-24). Such inducible expression systems, suitable for the control of transgene expression in cells or in mammals such as mice, include regulation by ecdysone, by estrogen, progesterone, tetracycline, chemical inducers of dimerization, and isopropyl-beta-D1 - thiogalactopyranoside (IPTG) (collectively referred to as "the regulatory molecule'). Each of these expression systems is well described in the literature and permits expression of the transgene throughout the animal in a manner controlled by the presence or absence of the regulatory molecule. For a review of inducible expression systems, see, *e.g.*, Mills, 2001, *Genes Devel.* 15:1461-1467, and references cited therein.

The regulatory elements referred to above include, but are not limited to, the cytomegalovirus hCMV immediate early gene, the early or late promoters of SV40 adenovirus (Bernoist *et al., Nature*, 290:304, 1981), the tet system, the lac system, the trp system, the TAC system, the TRC system, the major operator and promoter regions of phage A, the control regions of fd coat protein, the promoter for 3-phosphoglycerate kinase, the promoters of acid phosphatase, and the promoters of the yeast α-mating factors. Additional promoters include the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., *Cell* 22:787-797, 1988); the herpes thymidine kinase promoter (Wagner *et al., Proc. Natl. Acad. Sci. USA* 78:1441, 1981); or the regulatory sequences of the metallothionein gene (Brinster *et al., Nature* 296:39, 1988).

4. Assay for Testing Engineered RNA Precursors

Drosophila embryo lysates can be used to determine if an engineered RNA precursor was, in fact, the direct precursor of a mature stRNA or siRNA. This lysate assay is described in Tuschl et al., 1999, *supra*, Zamore *et al.*, 2000, *supra*, and Hutvdgner *et al.* 2001, *supra*. These lysates recapitulate RNAi *in vitro*, thus permitting investigation into whether the proposed precursor RNA was cleaved into a mature stRNA or siRNA by an RNAi-like mechanism. Briefly, the precursor RNA is incubated with Drosophila embryo lysate for various times, then assayed for the production of the

mature siRNA or stRNA by primer extension or Northern hybridization. As in the *in vivo* setting, mature RNA accumulates in the cell-free reaction. Thus, an RNA corresponding to the proposed precursor can be shown to be converted into a mature stRNA or siRNA duplex in the *Drosophila* embryo lysate.

Furthermore, an engineered RNA precursor can be functionally tested in the *Drosophila* embryo lysates. In this case, the engineered RNA precursor is incubated in the lysate in the presence of a 5' radiolabeled target mRNA in a standard *in vitro* RNAi reaction for various lengths of time. The target mRNA can be 5' radiolabeled using guanylyl transferase (as described in Tuschl *et al.*, 1999, *supr*a and references therein) or other suitable methods. The products of the *in vitro* reaction are then isolated and analyzed on a denaturing acrylamide or agarose gel to determine if the target mRNA has been cleaved in response to the presence of the engineered RNA precursor in the reaction. The extent and position of such cleavage of the mRNA target will indicate if the engineering of the precursor created a pre-siRNA capable of mediating sequence-specific RNAi.

III. Methods of Introducing RNAs, Vectors, and Host Cells

Physical methods of introducing nucleic acids include injection of a solution containing the RNA, bombardment by particles covered by the RNA, soaking the cell or organism in a solution of the RNA, or electroporation of cell membranes in the presence of the RNA. A viral construct packaged into a viral particle would accomplish both efficient introduction of an expression construct into the cell and transcription of RNA encoded by the expression construct. Other methods known in the art for introducing nucleic acids to cells may be used, such as lipid-mediated carrier transport, chemical-mediated transport, such as calcium phosphate, and the like. Thus the RNA may be introduced along with components that perform one or more of the following activities: enhance RNA uptake by the cell, inhibit annealing of single strands, stabilize the single strands, or other-wise increase inhibition of the target gene.

RNA may be directly introduced into the cell (*i.e.*, intracellularly); or introduced extracellularly into a cavity, interstitial space, into the circulation of an organism, introduced orally, or may be introduced by bathing a cell or organism in a solution

containing the RNA. Vascular or extravascular circulation, the blood or lymph system, and the cerebrospinal fluid are sites where the RNA may be introduced.

The cell with the target gene may be derived from or contained in any organism. The organism may a plant, animal, protozoan, bacterium, virus, or fungus. The plant may be a monocot, dicot or gymnosperm; the animal may be a vertebrate or invertebrate. Preferred microbes are those used in agriculture or by industry, and those that are pathogenic for plants or animals. Fungi include organisms in both the mold and yeast morphologies. Plants include arabidopsis; field crops (*e.g.*, alfalfa, barley, bean, com, cotton, flax, pea, rape, nice, rye, safflower, sorghum, soybean, sunflower, tobacco, and wheat); vegetable crops (*e.g.*, asparagus, beet, broccoli, cabbage, carrot, cauliflower, celery, cucumber, eggplant, lettuce, onion, pepper, potato, pumpkin, radish, spinach, squash, taro, tomato, and zucchini); fruit and nut crops (*e.g.*, almond, apple, apricot, banana, black- berry, blueberry, cacao, cherry, coconut, cranberry, date, faJoa, filbert, grape, grapefruit, guava, kiwi, lemon, lime, mango, melon, nectarine, orange, papaya, passion fruit, peach, peanut, pear, pineapple, pistachio, plum, raspberry, strawberry, tangerine, walnut, and watermelon); and ornamentals (*e.g.*, alder, ash, aspen, azalea, birch, boxwood, camellia, carnation, chrysanthemum, elm, fir, ivy, jasmine, juniper, oak, palm, poplar, pine, redwood, rhododendron, rose, and rubber). Examples of vertebrate animals include fish, mammal, cattle, goat, pig, sheep, rodent, hamster, mouse, rat, primate, and human; invertebrate animals include nematodes, other worms, drosophila, and other insects.

The skilled artisan will appreciate that the enumerated organisms are also useful for practicing other aspects of the invention, e.g., making transgenic organisms as described *infra*.

The cell having the target gene may be from the germ line or somatic, totipotent or pluripotent, dividing or non-dividing, parenchyma or epithelium, immortalized or transformed, or the like. The cell may be a stem cell or a differentiated cell. Cell types that are differentiated include adipocytes, fibroblasts, myocytes, cardiomyocytes, endothelium, neurons, glia, blood cells, megakaryocytes, lymphocytes, macrophages, neutrophils, eosinophils, basophils, mast cells, leukocytes, granulocytes, keratinocytes, chondrocytes, osteoblasts, osteoclasts, hepatocytes, and cells of the endocrine or exocrine glands.

Depending on the particular target gene and the dose of double stranded RNA material delivered, this process may provide partial or complete loss of function for the target gene. A reduction or loss of gene expression in at least 50%, 60%, 70%, 80%, 90%, 95% or 99% or more of targeted cells is exemplary. Inhibition of gene expression refers to the absence (or observable decrease) in the level of protein and/or mRNA product from a target gene. Specificity refers to the ability to inhibit the target gene without manifest effects on other genes of the cell. The consequences of inhibition can be confirmed by examination of the outward properties of the cell or organism (as presented below in the examples) or by biochemical techniques such as RNA solution hybridization, nuclease protection, Northern hybridization, reverse transcription, gene expression monitoring with a microarray, antibody binding, enzyme linked immunosorbent assay (ELISA), Western blotting, radioimmunoassay (RIA), other immunoassays, and fluorescence activated cell analysis (FACS).

For RNA-mediated inhibition in a cell line or whole organism, gene expression is conveniently assayed by use of a reporter or drug resistance gene whose protein product is easily assayed. Such reporter genes include acetohydroxyacid synthase (AHAS), alkaline phosphatase (AP), beta galactosidase (LacZ), beta glucoronidase (GUS), chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), horseradish peroxidase (HRP), luciferase (Luc), nopaline synthase (NOS), octopine synthase (OCS), and derivatives thereof. Multiple selectable markers are available that confer resistance to ampicillin, bleomycin, chloramphenicol, gentarnycin, hygromycin, kanamycin, lincomycin, methotrexate, phosphinothricin, puromycin, and tetracyclin. Depending on the assay, quantitation of the amount of gene expression allows one to determine a degree of inhibition which is greater than 10%, 33%, 50%, 90%, 95% or 99% as compared to a cell not treated according to the present invention. Lower doses of injected material and longer times after administration of an RNAi agent may result in inhibition in a smaller fraction of cells (*e.g.*, at least 10%, 20%, 50%, 75%, 90%, or 95% of targeted cells). Quantitation of gene expression in a cell may show similar amounts of inhibition at the level of accumulation of target mRNA or translation of target protein. As an example, the efficiency of inhibition may be determined by assessing the amount of gene product in the cell; mRNA may be detected with a hybridization probe having a nucleotide sequence outside the region used for the inhibitory double-stranded RNA, or

translated polypeptide may be detected with an antibody raised against the polypeptide sequence of that region.

The RNA may be introduced in an amount which allows delivery of at least one copy per cell. Higher doses (*e.g.*, at least 5, 10, 100, 500 or 1000 copies per cell) of material may yield more effective inhibition; lower doses may also be useful for specific applications.

IV. Methods of Treatment:

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant or unwanted target gene expression or activity. "Treatment", or "treating" as used herein, is defined as the application or administration of a therapeutic agent (*e.g.*, a RNAi agent or vector or transgene encoding same) to a patient, or application or administration of a therapeutic agent to an isolated tissue or cell line from a patient, who has a disease or disorder, a symptom of disease or disorder or a predisposition toward a disease or disorder, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve or affect the disease or disorder, the symptoms of the disease or disorder, or the predisposition toward disease.

With regards to both prophylactic and therapeutic methods of treatment, such treatments may be specifically tailored or modified, based on knowledge obtained from the field of pharmacogenomics. "Pharmacogenomics", as used herein, refers to the application of genomics technologies such as gene sequencing, statistical genetics, and gene expression analysis to drugs in clinical development and on the market. More specifically, the term refers the study of how a patient's genes determine his or her response to a drug (*e.g.*, a patient's "drug response phenotype", or "drug response genotype"). Thus, another aspect of the invention provides methods for tailoring an individual's prophylactic or therapeutic treatment with either the target gene molecules of the present invention or target gene modulators according to that individual's drug response genotype. Pharmacogenomics allows a clinician or physician to target prophylactic or therapeutic treatments to patients who will most benefit from the treatment and to avoid treatment of patients who will experience toxic drug-related side effects.

1. Prophylactic Methods

In one aspect, the invention provides a method for preventing in a subject, a disease or condition associated with an aberrant or unwanted target gene expression or activity, by administering to the subject a therapeutic agent (*e.g.*, a RNAi agent or vector or transgene encoding same). Subjects at risk for a disease which is caused or contributed to by aberrant or unwanted target gene expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the target gene aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of target gene aberrancy, for example, a target gene, target gene agonist or target gene antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

2. Therapeutic Methods

Another aspect of the invention pertains to methods of modulating target gene expression, protein expression or activity for therapeutic purposes. Accordingly, in an exemplary embodiment, the modulatory method of the invention involves contacting a cell capable of expressing target gene with a therapeutic agent (*e.g.*, a RNAi agent or vector or transgene encoding same) that is specific for the target gene or protein (*e.g.*, is specific for the mRNA encoded by said gene or specifying the amino acid sequence of said protein) such that expression or one or more of the activities of target protein is modulated. These modulatory methods can be performed *in vitro* (*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant or unwanted expression or activity of a target gene polypeptide or nucleic acid molecule. Inhibition of target gene activity is desirable in situations in which target gene is abnormally unregulated and/or in which decreased target gene activity is likely to have a beneficial effect.

3. Pharmacogenomics

The therapeutic agents (*e.g.*, a RNAi agent or vector or transgene encoding same) of the invention can be administered to individuals to treat (prophylactically or therapeutically) disorders associated with aberrant or unwanted target gene activity. In

conjunction with such treatment, pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, a physician or clinician may consider applying knowledge obtained in relevant pharmacogenomics studies in determining whether to administer a therapeutic agent as well as tailoring the dosage and/or therapeutic regimen of treatment with a therapeutic agent.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, for example, Eichelbaum, M. *et al.* (1996) *Clin. Exp. Pharmacol. Physiol.* 23(10-11): 983-985 and Linder, M.W. *et al.* (1997) *Clin. Chem.* 43(2):254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare genetic defects or as naturally-occurring polymorphisms. For example, glucose-6-phosphate dehydrogenase deficiency (G6PD) is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

One pharmacogenomics approach to identifying genes that predict drug response, known as "a genome-wide association", relies primarily on a high-resolution map of the human genome consisting of already known gene-related markers (*e.g.*, a "bi-allelic" gene marker map which consists of 60,000-100,000 polymorphic or variable sites on the human genome, each of which has two variants.) Such a high-resolution genetic map can be compared to a map of the genome of each of a statistically significant number of patients taking part in a Phase II/III drug trial to identify markers associated with a particular observed drug response or side effect. Alternatively, such a high resolution map can be generated from a combination of some ten-million known single nucleotide polymorphisms (SNPs) in the human genome. As used herein, a "SNP" is a common alteration that occurs in a single nucleotide base in a stretch of DNA. For example, a SNP may occur once per every 1000 bases of DNA. A SNP may

be involved in a disease process, however, the vast majority may not be disease-associated. Given a genetic map based on the occurrence of such SNPs, individuals can be grouped into genetic categories depending on a particular pattern of SNPs in their individual genome. In such a manner, treatment regimens can be tailored to groups of genetically similar individuals, taking into account traits that may be common among such genetically similar individuals.

Alternatively, a method termed the "candidate gene approach", can be utilized to identify genes that predict drug response. According to this method, if a gene that encodes a drugs target is known (*e.g.*, a target gene polypeptide of the present invention), all common variants of that gene can be fairly easily identified in the population and it can be determined if having one version of the gene versus another is associated with a particular drug response.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Alternatively, a method termed the "gene expression profiling", can be utilized to identify genes that predict drug response. For example, the gene expression of an animal dosed with a therapeutic agent of the present invention can give an indication whether gene pathways related to toxicity have been turned on.

Information generated from more than one of the above pharmacogenomics approaches can be used to determine appropriate dosage and treatment regimens for prophylactic or therapeutic treatment an individual. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a therapeutic agent, as described herein.

Therapeutic agents can be tested in an appropriate animal model. For example, an RNAi agent (or expression vector or transgene encoding same) as described herein can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with said agent. Alternatively, a therapeutic agent can be used in an animal model to determine the mechanism of action of such an agent. For example, an agent can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent can be used in an animal model to determine the mechanism of action of such an agent.

V. Pharmaceutical Compositions

The invention pertains to uses of the above-described agents for therapeutic treatments as described infra. Accordingly, the modulators of the present invention can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, antibody, or modulatory compound and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, intraperitoneal, intramuscular, oral (*e.g.*, inhalation), transdermal (topical), and transmucosal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyetheylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be

brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and

fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio

LD50/ED50. Compounds that exhibit large therapeutic indices are preferred. Although compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the EC50 (*i.e.*, the concentration of the test compound which achieves a half-maximal response) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

VI. Knockout and/or Knockdown Cells or Organisms

A further preferred use for the RNAi agents of the present invention (or vectors or transgenes encoding same) is a functional analysis to be carried out in eukaryotic cells, or eukaryotic non-human organisms, preferably mammalian cells or organisms and most preferably human cells, *e.g.* cell lines such as HeLa or 293 or rodents, *e.g.* rats and mice. By administering a suitable RNAi agent which is sufficiently complementary to a target mRNA sequence to direct target-specific RNA interference, a specific knockout or knockdown phenotype can be obtained in a target cell, *e.g.* in cell culture or in a target organism.

Thus, a further subject matter of the invention is a eukaryotic cell or a eukaryotic non-human organism exhibiting a target gene-specific knockout or knockdown phenotype comprising a fully or at least partially deficient expression of at least one endogeneous target gene wherein said cell or organism is transfected with at least one vector comprising DNA encoding an RNAi agent capable of inhibiting the expression of

the target gene. It should be noted that the present invention allows a target-specific knockout or knockdown of several different endogeneous genes due to the specificity of the RNAi agent.

Gene-specific knockout or knockdown phenotypes of cells or non-human organisms, particularly of human cells or non-human mammals may be used in analytic procedures, *e.g.* in the functional and/or phenotypical analysis of complex physiological processes such as analysis of gene expression profiles and/or proteomes. Preferably the analysis is carried out by high throughput methods using oligonucleotide based chips.

Using RNAi based knockout or knockdown technologies, the expression of an endogeneous target gene may be inhibited in a target cell or a target organism. The endogeneous gene may be complemented by an exogenous target nucleic acid coding for the target protein or a variant or mutated form of the target protein, *e.g.* a gene or a DNA, which may optionally be fused to a further nucleic acid sequence encoding a detectable peptide or polypeptide, *e.g.* an affinity tag, particularly a multiple affinity tag.

Variants or mutated forms of the target gene differ from the endogeneous target gene in that they encode a gene product which differs from the endogeneous gene product on the amino acid level by substitutions, insertions and/or deletions of single or multiple amino acids. The variants or mutated forms may have the same biological activity as the endogeneous target gene. On the other hand, the variant or mutated target gene may also have a biological activity, which differs from the biological activity of the endogeneous target gene, *e.g.* a partially deleted activity, a completely deleted activity, an enhanced activity etc. The complementation may be accomplished by compressing the polypeptide encoded by the endogeneous nucleic acid, *e.g.* a fusion protein comprising the target protein and the affinity tag and the double stranded RNA molecule for knocking out the endogeneous gene in the target cell. This compression may be accomplished by using a suitable expression vector expressing both the polypeptide encoded by the endogenous nucleic acid, *e.g.* the tag-modified target protein and the double stranded RNA molecule or alternatively by using a combination of expression vectors. Proteins and protein complexes which are synthesized *de novo* in the target cell will contain the exogenous gene product, *e.g.*, the modified fusion protein. In order to avoid suppression of the exogenous gene product by the RNAi agent, the nucleotide

sequence encoding the exogenous nucleic acid may be altered at the DNA level (with or without causing mutations on the amino acid level) in the part of the sequence which is homologous to the RNAi agent. Alternatively, the endogeneous target gene may be complemented by corresponding nucleotide sequences from other species, *e.g.* from mouse.

VII. Transgenic Organisms

Engineered RNA precursors of the invention can be expressed in transgenic animals. These animals represent a model system for the study of disorders that are caused by, or exacerbated by, overexpression or underexpression (as compared to wildtype or normal) of nucleic acids (and their encoded polypeptides) targeted for destruction by the RNAi agents, e.g., siRNAs and shRNAs, and for the development of therapeutic agents that modulate the expression or activity of nucleic acids or polypeptides targeted for destruction.

Transgenic animals can be farm animals (pigs, goats, sheep, cows, horses, rabbits, and the like), rodents (such as rats, guinea pigs, and mice), non-human primates (for example, baboons, monkeys, and chimpanzees), and domestic animals (for example, dogs and cats). Invertebrates such as Caenorhabditis elegans or Drosophila can be used as well as non-mammalian vertebrates such as fish (e.g., zebrafish) or birds (e.g., chickens).

Engineered RNA precursors with stems of 18 to 30 nucleotides in length are preferred for use in mammals, such as mice. A transgenic founder animal can be identified based upon the presence of a transgene that encodes the new RNA precursors in its genome, and/or expression of the transgene in tissues or cells of the animals, for example, using PCR or Northern analysis. Expression is confirmed by a decrease in the expression (RNA or protein) of the target sequence.

A transgenic founder animal can be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding the RNA precursors can further be bred to other transgenic animals carrying other transgenes. In addition, cells obtained from the transgenic founder animal or its offspring can be cultured to establish primary, secondary, or immortal cell lines containing the transgene.

1. Procedures for Making Transgenic, Non-Human Animals

A number of methods have been used to obtain transgenic, non-human animals, which are animals that have gained an additional gene by the introduction of a transgene into their cells (e.g., both the somatic and genn cells), or into an ancestor's genn line. In some cases, transgenic animals can be generated by commercial facilities (e.g., The Transgenic Drosophila Facility at Michigan State University, The Transgenic Zebrafish Core Facility at the Medical College of Georgia (Augusta, Georgia), and Xenogen Biosciences (St. Louis, MO). In general, the construct containing the transgene is supplied to the facility for generating a transgenic animal.

Methods for generating transgenic animals include introducing the transgene into the germ line of the animal. One method is by microinjection of a gene construct into the pronucleus of an early stage embryo (e.g., before the four-cell stage; Wagner et al., 1981, Proc. Natl. Acad. Sci. USA 78:5016; Brinster et al., 1985, Proc. Natl. Acad. Sci. USA 82:4438). Alternatively, the transgene can be introduced into the pronucleus by retroviral infection. A detailed procedure for producing such transgenic mice has been described (see e.g., Hogan et al., MP1 ulating the Mouse ErnbnLo. Cold Spring Harbour Laboratory, Cold Spring Harbour, NY (1986); U.S. Patent No. 5,175,383 (1992)). This procedure has also been adapted for other animal species (e.g., Hammer et al., 1985, Nature 315:680; Murray et al., 1989, Reprod. Fert. Devl. 1:147; Pursel et al., 1987, Vet. hnmunol. Histopath. 17:303; Rexroad et al., 1990, J. Reprod. Fert. 41 (suppl): 1 19; Rexroad et al., 1989, Molec. Reprod. Devl. 1:164; Simons et al., 1988, BioTechnology 6:179; Vize et al., 1988, J. Cell. Sci. 90:295; and Wagner, 1989, J. Cell. Biochem. 13B (suppl): 164).

In brief, the procedure involves introducing the transgene into an animal by microinjecting the construct into the pronuclei of the fertilized mammalian egg(s) to cause one or more copies of the transgene to be retained in the cells of the developing marmnal(s). Following introduction of the transgene construct into the fertilized egg, the egg may be incubated in vitro for varying amounts of time, or reimplanted a in surrogate host, or both. One common method is to incubate the embryos in vitro for about 1-7 days, depending on the species, and then reimplant them into the surrogate host. The presence of the transgene in the progeny of the transgenically manipulated embryos can be tested by Southern blot analysis of a segment of tissue.

Another method for producing germ-line transgenic animals is through the use of embryonic stem (ES) cells. The gene construct can be introduced into embryonic stem cells by homologous recombination (Thomas et al., 1987, Cell 51:503; Capecchi, Science 1989, 244:1288; Joyner et al., 1989, Nature 338:153) in a transcriptionally active region of the genome. A suitable construct can also be introduced into embryonic stem cells by DNA-mediated transfection, such as by 17 electroporation (Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, 1987). Detailed procedures for culturing embryonic stem cells (e.g., ES-D3@ ATCC# CCL-1934, ES-El4TG2a, ATCC# CCL-1821, American Type Culture Collection, Rockville, AM) and methods of making transgenic animals from embryonic stem cells can be found in Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, ed. E.J. Robertson (IRL Press, 1987). In brief, the ES cells are obtained from pre-implantation embryos cultured in vitro (Evans et al., 1981, Nature 292:154-156). Transgenes can be efficiently introduced into ES cells by DNA transfection or by retrovirus-mediated transduction. The resulting transformed ES cells can thereafter be combined with blastocysts from a non-human animal. The ES cells colonize the embryo and contribute to the genn line of the resulting chimeric animal.

In the above methods, the transgene can be introduced as a linear construct, a circular plasmid, or a viral vector, which can be incorporated and inherited as a transgene integrated into the host genome. The transgene can also be constructed to permit it to be inherited as an extrachromosomal plasmid (Gassmann et al., 1995, Proc. Natl. Acad. Sci. USA 92:1292). A plasmid is a DNA molecule that can replicate autonomously in a host.

The transgenic, non-human animals can also be obtained by infecting or transfecting cells either in vivo (e.g., direct injection), ex vivo (e.g., infecting the cells outside the host and later reimplanting), or in vitro (e.g., infecting the cells outside host), for example, with a recombinant viral vector carrying a gene encoding the engineered RNA precursors. Examples of suitable viral vectors include recombinant retroviral vectors (Valerio et al., 1989, Gene 84:419; Scharfinan et al., 1991, Proc. Natl. Acad. Sci. USA 88:462; Miller and Buttimore, 1986, Mol. Cell. Biol. 6:2895), recombinant adenoviral vectors (Freidman et al., 1986, Mol. Cell. Biol. 6:3791; Levrero et al., 1991, Gene 101: 195), and recombinant Herpes simplex viral vectors (Fink et al., 1992,

Human Gene Therapy 3:11). Such methods are also useful for introducing constructs into cells for uses other than generation of transgenic animals.

Other approaches include insertion of transgenes encoding the new engineered RNA precursors into viral vectors including recombinant adenovirus, adenoassociated virus, and herpes simplex virus-1, or recombinant bacterial or eukaryotic plasmids. Viral vectors transfect cells directly. Other approaches include delivering the transgenes, in the form of plasmid DNA, with the help of, for example, cationic liposornes (lipofectin) or derivatized (e.g. antibody conjugated) polylysine conjugates, gramacidin S, artificial viral envelopes, or other such intracellular carriers, as well as direct injection of the transgene construct or $CaPO_4$ precipitation carried out *in vivo*. Such methods can also be used in vitro to introduce constructs into cells for uses other than generation of transgenic animals.

Retrovirus vectors and adeno-associated virus vectors can be used as a recombinant gone delivery system for the transfer of exogenous genes in vivo or in vitro. These vectors provide efficient delivery of genes into cells, and the transferred nucleic acids are stably integrated into the chromosomal DNA of the host. The development of specialized cell lines (termed "packaging cells") which produce only replication-defective retroviruses has increased the utility of retroviruses for gene therapy, and defective retroviruses are characterized for use in gene transfer for gene therapy purposes (for a review see Miller, 1990, Blood 76:271). A replication defective retrovirus can be packaged into virions which can be used to infect a target cell through the use of a helper virus by standard techniques. Protocols for producing recombinant retroviruses and for infecting cells in vitro or in vivo with such viruses can be found in Current Protocols in Molecular Biology, Ausubel, F.M. et al., (eds.) Greene Publishing Associates, (1989), Sections 9 9.14 and other standard laboratory manuals.

Examples of suitable retroviruses include pLJ, pZIP, pWE and pEM which are known to those skilled in the art. Examples of suitable packaging virus lines for preparing both ecotropic and amphotropic retroviral systems include Psi-Crip, PsiCre, Psi-2 and Psi-Am. Retroviruses have been used to introduce a variety of genes into many different cell types, including epithelial cells, in vitro and/or in vivo (see for example Eglitis, et al., 1985, Science 230:1395-1398; Danos and Mulligan, 1988, Proc. NatI. Acad. Sci. USA 85:6460-6464; Wilson et al., 1988, Proc. NatI. Acad. Sci. USA

85:3014-3018; Armentano et al., 1990, Proc. NatI. Acad. Sci. USA 87:61416145; Huber et al., 1991, Proc. NatI. Acad. Sci. USA 88:8039-8043; Ferry et al., 1991, Proc. NatI. Acad. Sci. USA 88:8377-8381; Chowdhury et al., 1991, Science 254:1802-1805; van Beusechem. et al., 1992, Proc. Nad. Acad. Sci. USA 89:7640-19 ; Kay et al., 1992, Human Gene Therapy 3:641-647; Dai et al., 1992, Proc. Natl. Acad. Sci. USA 89:10892-10895; Hwu et al., 1993, J. Immunol. 150:4104-4115; U.S. Patent No. 4,868,116; U.S. Patent No. 4,980,286; PCT Application WO 89/07136; PCT Application WO 89/02468; PCT Application WO 89/05345; and PCT Application WO 92/07573).

In another example, recombinant retroviral vectors capable of transducing and expressing genes inserted into the genome of a cell can be produced by transfecting the recombinant retroviral genome into suitable packaging cell lines such as PA317 and Psi-CRIP (Comette et al., 1991, Human Gene Therapy 2:5-10; Cone et al., 1984, Proc. Natl. Acad. Sci. USA 81:6349). Recombinant adenoviral vectors can be used to infect a wide variety of cells and tissues in susceptible hosts (e.g., rat, hamster, dog, and chimpanzee) (Hsu et al., 1992, J. Infectious Disease, 166:769), and also have the advantage of not requiring mitotically active cells for infection. Another viral gene delivery system useful in the present invention also utilizes adenovirus-derived vectors. The genome of an adenovirus can be manipulated such that it encodes and expresses a gene product of interest but is inactivated in terms of its ability to replicate in a normal lytic viral life cycle. See, for example, Berkner et al. (1988, BioTechniques 6:616), Rosenfeld et al. (1991, Science 252:431-434), and Rosenfeld et al. (1992, Cell 68:143-155). Suitable adenoviral vectors derived from the adenovirus strain Ad type 5 d1324 or other strains of adenovirus (e.g., Ad2, AO, Ad7 etc.) are known to those skilled in the art. Recombinant adenoviruses can be advantageous in certain circumstances in that they are not capable of infecting nondividing cells and can be used to infect a wide variety of cell types, including epithelial cells (Rosenfeld et al.,1992, cited supra). Furthermore, the virus particle is relatively stable and amenable to purification and concentration, and as above, can be modified to affect the spectrum of infectivity. Additionally, introduced adenoviral DNA (and foreign DNA contained therein) is not integrated into the genome of a host cell but remains episomal, thereby avoiding potential problems that can occur as a result of insertional mutagenesis hz situ where introduced DNA becomes integrated into the host genome (e.g., retroviral DNA). Moreover, the carrying capacity of the adenoviral genome for foreign DNA is large (up to 8 kilobases) relative to other gene

delivery vectors (Berkner et al. cited supra; Haj-Ahmand and Graham, 1986, J. Virol. 57:267).

Yet another viral vector system useful for delivery of the subject transgenes is the adeno-associated virus (AAV). Adeno-associated virus is a naturally occurring defective virus that requires another virus, such as an adenovirus or a herpes virus, as a helper virus for efficient replication and a productive life cycle. For a review, see Muzyczka et al. (1992, Curr. Topics in Micro.and Immunol. 158:97-129). It is also one of the few viruses that may integrate its DNA into non-dividing cells, and exhibits a high frequency of stable integration (see for example Flotte et al. (1992, Am. J. Respir. Cell. Mol. Biol. 7:349-356; Samulski et al., 1989, J. Virol. 63:3822-3828; and McLaughlin et al. (1989, J. Virol. 62:1963-1973). Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate. Space for exogenous DNA is limited to about 4.5 kb. An AAV vector such as that described in Tratschin et al. (1985) MoL Cell. Biol. 5:3251-3260 can be used to introduce DNA into cells. A variety of nucleic acids have been introduced into different cell types using AAV vectors (see for example Hennonat et al. (1984) Proc. Nad. Acad. Sci. USA 8 1:64666470; Tratschin et al. (1985) Mol. Cell. BioL 4:2072-2081; Wondisford et al. (1988) MoL EndocrinoL 2:32-39; Tratschin et al. (1984) J ViroL 51:611-619; and Flotte et al. (1993) J BioL Chem. 268:3781-3790).

In addition to viral transfer methods, such as those illustrated above, non-viral methods can also be employed to cause expression of an shRNA or engineered RNA precursor of the invention in the tissue of an animal. Most non-viral methods of gene transfer rely on nonnal mechanisms used by mammalian cells for the uptake and intracellular transport of macromolecules. In preferred embodiments, non-viral gene delivery systems of the present invention rely on endocytic pathways for the uptake of the subject gene of the invention by the targeted cell. Exemplary gene delivery systems of this type include liposomal derived systems, poly-lysine conjugates, and artificial viral envelopes. Other embodiments include plasmid injection systems such as are described in Meuli et al., (2001) J Invest. DerinatoL, 116(l):131-135; Cohen et al., (2000) Gene Ther., 7(22):1896-905; and Tam et al., (2000) Gene Ther., 7(21):186774.

In a representative embodiment, a gene encoding an shRNA or engineered RNA precursor of the invention can be entrapped in liposomes bearing positive charges on their surface (e.g., lipofectins) and (optionally) which are tagged with antibodies against

cell surface antigens of the target tissue (Mizuno et al., (1992) No Shinkei Geka, 20:547-55 1; PCT publication WO91/06309; Japanese patent application 10473 8 1; and European patent publication EP-A-43 075).

Animals harboring the transgene can be identified by detecting the presence of the transgene in genomic DNA (e.g., using Southern analysis). In addition, expression of the shRNA or engineered RNA precursor can be detected directly (e.g., by Northern analysis). Expression of the transgene can also be confirmed by detecting a decrease in the amount of protein corresponding to the targeted sequence. When the transgene is under the control of an inducible or developmentally regulated promoter, expression of the target protein is decreased when the transgene is induced or at the developmental stage when the transgene is expressed, respectively.

2. Clones of Transgenic Animals

Clones of the non-human transgenic animals described herein can be produced according to the methods described in Wilmut et al. ((1997) Nature, 385:810-813) and PCT publication Nos. WO 97/07668 and WO 97/07669. In brief, a cell, *e.g.*, a somatic cell from the transgenic animal, can be isolated and induced to exit the growth cycle and enter the G0 phase to become quiescent. The quiescent cell can then be fused, *e.g.*, through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops into a morula or blastocyte and is then transferred to a pseudopregnant female foster animal. Offspring borne of this female foster animal will be clones of the animal from which the cell, e.g., the somatic cell, was isolated.

Once the transgenic animal is produced, cells of the transgenic animal and cells from a control animal are screened to determine the presence of an RNA precursor nucleic acid sequence, e.g., using polymerase chain reaction (PCR). Alternatively, the cells can be screened to determine if the RNA precursor is expressed (e.g., by standard procedures such as Northern blot analysis or reverse transcriptase-polymerase chain reaction (RT-PCR); Sambrook et al., Molecular Cloning - A Laboratory Manual, (Cold Spring Harbor Laboratory, 1989)).

The transgenic animals of the present invention can be homozygous or heterozygous, and one of the benefits of the invention is that the target mRNA is effectively degraded even in heterozygotes. The present invention provides for

transgenic animals that carry a transgene of the invention in all their cells, as well as animals that carry a transgene in some, but not all of their cells. That is, the invention provides for mosaic animals. The transgene can be integrated as a single transgene or in concatatners, e.g., head-to-head tandems or head-to-tail tandems.

For a review of techniques that can be used to generate and assess transgenic animals, skilled artisans can consult Gordon (IwL Rev. CytoL 1 1 5:171-229, 1989), and may obtain additional guidance from, for example: Hogan et al. "Manipulating the Mouse Embryo" (Cold Spring Harbor Press, Cold Spring Harbor, NY, 1986; Krimpenfort et al., BiolTechnology 9:86, 1991; Palmiter et al., Cell 41:343, 1985; Kraemer et al., "Genetic Manipulation of the Early Mammalian Embryo," Cold Spring Harbor Press, Cold Spring Harbor, NY, 1985; Hammer et al., Nature 315:680, 1985; Purcel et al., Scieizce, 244:1281, 1986; Wagner et al., U.S. Patent No. 5,175,385; and Krimpenfort et al., U.S. Patent No. 5,175,384.

3. Transgenic Plants

Among the eukaryotic organisms featured in the invention are plants containing an exogenous nucleic acid that encodes an engineered RNA precursor of the invention.

Accordingly, a method according to the invention comprises making a plant having a nucleic acid molecule or construct, e.g., a transgene, described herein. Techniques for introducing exogenous micleic acids into monocotyledonous and dicotyledonous plants are known in the art, and include, without limitation, Agrobacterium-mediated transformation, viral vector-mediated transformation, electroporation and particle gun transformation, see, e.g., U.S. Patents Nos. 5,204,253 and 6,013,863. If a cell or tissue culture is used as the recipient tissue for transformation, plants can be regenerated from transformed cultures by techniques known to those skilled in the art. Transgenic plants can be entered into a breeding program, e.g., to introduce a nucleic acid encoding a polypeptide into other lines, to transfer the nucleic acid to other species or for further selection of other desirable traits. Alternatively, transgenic plants can be propagated vegetatively for those species amenable to such techniques. Progeny includes descendants of a particular plant or plant line. Progeny of a plant include seeds formed on F1, F2, F3, and subsequent generation plants, or seeds formed on BQ, BC2, BC3, and subsequent generation plants. Seeds produced by a

transgenic plant can be grown and then selfed (or outcrossed and selfed) to obtain seeds homozygous for the nucleic acid encoding a novel polypeptide.

A suitable group of plants with which to practice the invention include dicots, such as safflower, alfalfa, soybean, rapeseed (high erucic acid and canola), or sunflower. Also suitable are monocots such as corn, wheat, rye, barley, oat, rice, millet, amaranth or sorghum. Also suitable are vegetable crops or root crops such as potato, broccoli, peas, sweet corn, popcorn, tomato, beans (including kidney beans, lima beans, dry beans, green beans) and the like. Also suitable are fruit crops such as peach, pear, apple, cherry, orange, lemon, grapefruit, plum, mango and palm. Thus, the invention has use over a broad range of plants, including species from the genera Anacardium, Arachis, Asparagus, Atropa, Avena, Brassica, Citrus, Citrullus, Capsicum, Carthamus, Cocos, Coffea, Cucumis, Cucurbita, Daucus, Elaeis, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyalnus, Lactuca, Linum, Lolium, Lupinus, Lycopersicon, Malus, Manihot, Majorana, Medicago, Nicotiana, Olea, Oryza, Panicum, Pannesetum, Persea, Phaseolus, Pistachia, Pisum, Pyrus, Prunus, Raphanus, Ricinus, Secale, Senecio, Sinapis, Solanum, Sorghum, Theobromus, Trigonella, Triticum, Vicia, Vitis, Vigna and Zea.

The skilled artisan will appreciate that the enumerated organisms are also useful for practicing other aspects of the invention, e.g., as host cells, as described *supra*.

The nucleic acid molecules of the invention can be expressed in plants in a cell- or tissue-specific manner according to the regulatory elements chosen to include in a particular nucleic acid construct present in the plant. Suitable cells, tissues, and organs in which to express a chimeric polypeptide of the invention include, without limitation, egg cell, central cell, synergid cell, zygote, ovule primordia, nucellus, integuments, endothelium, female garnetophyte cells, embryo, axis, cotyledons, suspensor, endosperm, seed coat, ground meristem, vascular bundle, cambium, phloem, cortex, shoot or root apical meristems, lateral shoot or root meristems, floral meristem, leaf primordia, leaf mesophyll cells, and leaf epidermal cells, e.g., epidermal cells involved in fortning the cuticular layer. Also suitable are cells and tissues grown in liquid media or on semi-solid media.

4. Transgenic Fungi

Other eukaryotic organisms featured in the invention are fungi containing an exogenous nucleic acid molecule that encodes an engineered RNA precursor of the invention. Accordingly, a method according to the invention comprises introducing a nucleic acid molecule or construct as described herein into a fungus. Techniques for introducing exogenous nucleic acids into many fungi are known in the art, see, e.g., U.S. Patents Nos. 5,252,726 and 5,070,020. Transformed fungi can be cultured by techniques known to those skilled in the art. Such fungi can be used to introduce a nucleic acid encoding a polypeptide into other fungal strains, to transfer the nucleic acid to other species or for ftirther selection of other desirable traits.

A suitable group of fimgi with which to practice the invention include fission yeast and budding yeast, such as Saccharoinyces cereviseae, S. pombe, S. carlsbergeris and Candida albicans. Filamentous fungi such as Aspergillus spp. and Penicillium spp. are also useful.

VIII. Functional Genomics and/or Proteomics

Preferred applications for the cell or organism of the invention is the analysis of gene expression profiles and/or proteomes. In an especially preferred embodiment an analysis of a variant or mutant form of one or several target proteins is carried out, wherein said variant or mutant forms are reintroduced into the cell or organism by an exogenous target nucleic acid as described above. The combination of knockout of an endogeneous gene and rescue by using mutated, *e.g.* partially deleted exogenous target has advantages compared to the use of a knockout cell. Further, this method is particularly suitable for identifying functional domains of the targeted protein. In a further preferred embodiment a comparison, *e.g.* of gene expression profiles and/or proteomes and/or phenotypic characteristics of at least two cells or organisms is carried out. These organisms are selected from: (i) a control cell or control organism without target gene inhibition, (ii) a cell or organism with target gene inhibition and (iii) a cell or organism with target gene inhibition plus target gene complementation by an exogenous target nucleic acid.

Furthermore, the RNA knockout complementation method may be used for is preparative purposes, *e.g.* for the affinity purification of proteins or protein complexes from eukaryotic cells, particularly mammalian cells and more particularly human cells. In this embodiment of the invention, the exogenous target nucleic acid preferably codes for a target protein which is fused to art affinity tag. This method is suitable for functional proteome analysis in mammalian cells, particularly human cells.

Another utility of the present invention could be a method of identifying gene function in an organism comprising the use of an RNAi agent to inhibit the activity of a target gene of previously unknown function. Instead of the time consuming and laborious isolation of mutants by traditional genetic screening, functional genomics would envision determining the function of uncharacterized genes by employing the invention to reduce the amount and/or alter the timing of target gene activity. The invention could be used in determining potential targets for pharmaceutics, understanding normal and pathological events associated with development, determining signaling pathways responsible for postnatal development/aging, and the like. The increasing speed of acquiring nucleotide sequence information from genomic and expressed gene sources, including total sequences for the yeast, *D. melanogaster*, and *C. elegans* genomes, can be coupled with the invention to determine gene function in an organism (*e.g.*, nematode). The preference of different organisms to use particular codons, searching sequence databases for related gene products, correlating the linkage map of genetic traits with the physical map from which the nucleotide sequences are derived, and artificial intelligence methods may be used to define putative open reading frames from the nucleotide sequences acquired in such sequencing projects. A simple assay would be to inhibit gene expression according to the partial sequence available from an expressed sequence tag (EST). Functional alterations in growth, development, metabolism, disease resistance, or other biological processes would be indicative of the normal role of the EST's gene product.

The ease with which RNA can be introduced into an intact cell/organism containing the target gene allows the present invention to be used in high throughput screening (HTS). Solutions containing RNAi agents that are capable of inhibiting the different expressed genes can be placed into individual wells positioned on a microtiter plate as an ordered array, and intact cells/organisms in each well can be assayed for any changes or modifications in behavior or development due to inhibition of target gene

activity. The amplified RNA can be fed directly to, injected into, the cell/organism containing the target gene. Alternatively, the RNAi agent can be produced from a vector, as described herein. Vectors can be injected into, the cell/organism containing the target gene. The function of the target gene can be assayed from the effects it has on the cell/organism when gene activity is inhibited. This screening could be amenable to small subjects that can be processed in large number, for example: arabidopsis, bacteria, drosophila, fungi, nematodes, viruses, zebrafish, and tissue culture cells derived from mammals. A nematode or other organism that produces a colorimetric, fluorogenic, or luminescent signal in response to a regulated promoter (*e.g.*, transfected with a reporter gene construct) can be assayed in an HTS format.

The present invention may be useful in allowing the inhibition of essential genes. Such genes may be required for cell or organism viability at only particular stages of development or cellular compartments. The functional equivalent of conditional mutations may be produced by inhibiting activity of the target gene when or where it is not required for viability. The invention allows addition of RNAi agent at specific times of development and locations in the organism without introducing permanent mutations into the target genome.

IX. Screening Assays

The methods of the invention are also suitable for use in methods to identify and/or characterize potential pharmacological agents, *e.g.* identifying new pharmacological agents from a collection of test substances and/or characterizing mechanisms of action and/or side effects of known pharmacological agents.

Thus, the present invention also relates to a system for identifying and/or characterizing pharmacological agents acting on at least one target protein comprising: (a) a eukaryotic cell or a eukaryotic non- human organism capable of expressing at least one endogeneous target gene coding for said so target protein, (b) at least one RNAi agent molecule capable of inhibiting the expression of said at least one endogeneous target gene, and (c) a test substance or a collection of test substances wherein pharmacological properties of said test substance or said collection are to be identified and/or characterized. Further, the system as described above preferably comprises: (d) at least one exogenous target nucleic acid coding for the target protein or a variant or mutated form of the target protein wherein said exogenous target nucleic acid differs

from the endogeneous target gene on the nucleic acid level such that the expression of the exogenous target nucleic acid is substantially less inhibited by the RNAi agent than the expression of the endogeneous target gene.

The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S. (1997) *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), chips (Fodor (1993) Nature 364:555-556), bacteria (Ladner USP 5,223,409), spores (Ladner USP '409), plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and Smith (1990) *Science* 249:386-390); (Devlin (1990) *Science* 249:404-406); (Cwirla *et al.* (1990) *Proc. Natl. Acad. Sci.* 87:6378-6382); (Felici (1991) *J. Mol. Biol.* 222:301-310); (Ladner supra.)).

In a preferred embodiment, the library is a natural product library, *e.g.*, a library produced by a bacterial, fungal, or yeast culture. In another preferred embodiment, the library is a synthetic compound library.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patents and published patent applications cited throughout this application are incorporated herein by reference.

EXAMPLES

Example I: Functionally asymmetric siRNA duplexes

To assess quantitatively if the two strands of an siRNA duplex are equally competent to direct RNAi, the individual rates of sense and anti-sense target cleavage for an siRNA duplex directed against the firefly luciferase mRNA were examined (Figure 1A). The relevant portions of the sense and anti-sense target RNA sequences are shown in Figure 1A and the siRNA sequence in Figure 1B. This siRNA duplex effectively silences firefly luciferase expression in culture human HeLa cells. Using a *Drosophila* embryo-derived *in vitro* RNAi reaction, a significant difference in the rate of target cleavage for the two siRNA strands was found; the anti-sense siRNA strand directed more efficient RNAi against a sense RNA target than the sense siRNA strand for an anti-sense target (Figure 1B). (Anti-sense siRNA strands and sense target RNAs are always shown in black, and sense siRNAs and anti-sense targets, in grey). Control experiments showed that using siRNA duplexes with 5' phosphates did not alter this result (data not shown), indicating that different rates of phosphorylation for the two strands is not the cause for the observed asymmetry. Surprisingly, the two stands of the luciferase duplex siRNA duplex, used individually as 5' phosphorylated single stands, had identical rates of target cleavage (Figure 1C). RNAi directed by single-stranded siRNA is roughly 10-fold less efficient than that triggered by siRNA duplexes, reflecting the ~ 100-fold lower stability of single-stranded siRNAs *in vitro* and *in vivo* (Schwarz et al., 2002). The difference in the rate of cleavage directed by the sense and anti-sense strands when the reaction was programmed with an siRNA duplex is unlikely to reflect a difference in the inherent susceptibility of the two targets to RNAi. Instead, the observation that the same two siRNA strands are equally effective as single-strands, but show dramatically different activities when paired with each other, indicates that the asymmetry in their function is established at a step in the RNAi pathway prior to the encounter of the programmed RISC with its corresponding RNA target.

Example II: Differential RISC assembly accounts for siRNA strand functional asymmetry

To identify the source of asymmetry in the function of this siRNA duplex, the unwinding of the two siRNA strands when the duplex was incubated in a standard *in vitro* RNAi reaction was measured. This assay was shown previously to determine accurately the fraction of siRNA that is unwound in an ATP-dependent step in the RNAi pathway; no functional RISC is assembled in the absence of ATP (Nykänen et al., 2001). Previous studies show that siRNA unwinding correlates with capacity of an siRNA to function in target cleavage (Nykänen et al., 2001; Martinez et al., 2002), demonstrating that siRNA duplex unwinding is required to assemble a RISC competent to base pair with its target RNA. Here, the accumulation of single standed siRNA from the luciferase siRNA duplex after 1 hour incubation in an *in vitro* RNAi reaction in the absence of target RNA was measured. After one hour of incubation with *Drosophila* embryo lysate in a standard RNAi reaction, 22% of the anti-sense strand of the luciferase siRNA was converted to single-strand (Figure 1D; 'siRNA B' solid black bar). Remarkably, a corresponding amount of single-stranded sense siRNA was not detected. Instead, only 3% of the sense strand accumulated as single-stranded siRNA (Figure 1D; 'siRNA B' solid grey bar). In control experiments, no single-stranded RNA was detected without incubation in lysate (not shown), demonstrating that the siRNA was entirely double-stranded at the beginning of the reaction. Since the production of single-stranded anti-sense siRNA must be accompanied by an equal amount of single-stranded sense siRNA, the missing sense-strand must have been destroyed after unwinding.

To establish that the observed asymmetry in the accumulation of the two single-strands was not an artifact of our unwinding assay, an independent method for measuring the fraction of siRNA present as single-strands in protein-RNA complexes was. In this assay, double-stranded siRNA was incubated with *Drosophila* embryo lysate in a standard RNAi reaction for 1 h, then a 31 nt 2′-O-methyl RNA oligonucleotide containing a 21 nt sequence complementary to the radiolabeled siRNA strand was added. 2′-O-methyl oligonucleotides are not cleaved by the RNAi machinery, but can bind stably to complementary siRNA within the RISC (Martin Simard, GH, Craig Mello, and PDZ, manuscript in preparation). To allow recovery of RISC, the 2′-O-methyl oligonucleotide was tethered to a magnetic bead via a biotin-streptavidin linkage. After washing away unbound RNA and protein, the amount of radioactive siRNA bound to the bead was measured. The assay was performed with separate siRNA duplexes in which either the sense or the anti-sense strand was 5′-^{32}P-radiolabeled. Capture of ^{32}P-

siRNA was observed when the 2′-*O*-methyl oligonucleotide contained a 21-nt region complementary to the radiolabeled siRNA strand, but not when an unrelated oligonucleotide was used. The assay captures all RISC activity directed by the siRNA strand complementary to the tethered oligonucleotide, demonstrating that it measures siRNA present in the lysate as single-strand complexed with RISC proteins. This assay recapitulates the results of the unwinding assay described above: for the siRNA in Figure 1D; 'si RNA B' open bars, nearly ten-fold more anti-sense siRNA was detected than sense strand. An explanation for these results is that the two strands of this siRNA duplex are differentially loaded into the RISC, and that single-stranded siRNA not assembled into RISC is degraded. Functional asymmetry occurred only when the trigger siRNA was double-stranded, not when the two siRNA strands were tested individually (Fig. 1B and 1C). Thus, asymmetric assembly of RISC was a feature of the siRNA duplex, rather than of either the sequences of the individual siRNA strands or the accessibility of the targeted sites to cleavage.

Example III: Base-pairing at the 5′ end of the siRNA strand gates RISC assembly

The finding that the two siRNA strands can have different capacities to form RISC when paired in a duplex indicates that some feature of the 19 base-pairs of the duplex determines functional asymmetry. These base-pairs must be disrupted to produce RISC (Nykänen et al., 2001), which contains single-stranded siRNA (Martinez et al., 2002). The siRNAs used in Figure 1B were examined for base-pairing features that might distinguish the two siRNA strands. For the siRNA in Figure 1B, the 5′ end of the anti-sense siRNA strand begins with U and is thus paired to the sense siRNA strand by an A:U base pair (2 hydrogen bonds). In contrast, the 5′ nucleotide of the sense siRNA strand is linked to the anti-sense strand by a C:G base pair (3 hydrogen bonds). The sense siRNA strand forms 8-10-fold less RISC and guides cleavage of its RNA target at a correspondingly slower rate than the anti-sense strand. A working hypothesis to explain the observed functional asymmetry is that the siRNA strand whose 5′ end is more weakly bound to the complementary strand more readily incorporates into RISC. In this view, the relative base-pairing strengths of the 5′ ends of the two siRNA strands would determine their relative extents of RISC formation.

As an initial test of this idea, the 5′ nucleotide of the siRNA sense strand was changed from C to U (Figure 1E). This changed the base pair formed between the 5′ most nucleotide of the sense strand and position 19 of the anti-sense strand from the Watson-Crick base pair C:G to the weaker, less stable wobble pair U:G, while leaving the anti-sense strand of the siRNA unaltered. Remarkably, the change of this single nucleotide not only enhanced the rate of cleavage directed by the sense strand, but virtually eliminated the ability of the anti-sense strand to direct RNAi (Figure 1E).

To determine the basis for the reversed functional asymmetry for the siRNA in Figure 1E, the amount of each strand that was single stranded after incubation of the siRNA duplex in *Drosphilia* embryo lystae was determined. After 1h, nearly 30% of the sense siRNA strand was converted to single stranded, but no single-stranded anti-sense strand was detected (Figure 1D; 'siRNA E'). Therefore, the simplest explanation for the asymmetric function of this siRNA is that the sense strand, but not the anti-sense, of this siRNa duplex was incorporated into RISC. Thus, a single nucleotide mutation in the sense siRNA strand of the siRNA in Figure 1B completely reversed the relative abilites of the two strands to assemble in the enzyme complex that directs RNAi.

The stability of the initial five base pairs of the siRNA strands was claculated in Figure 1 using the nearest-neighbor method and the mfold algorithm (D.H. Mathews, 1999; Zuker, 2003). The 5′ end of the sense siRNA strand in Figure 1E, but not that in 1B, is predicted to exist as an equilibrium of two conformers of nearly equal energy (Figure 10). In one conformer, the 5′ nucleotide of the sense strand is bound to the anti-sense strand by a U:G wobble pair, whereas in the other conformer the 5′ end of this siRNA strand is unpaired. The analysis suggests that RISC assembly favors the siRNA strand whose 5′ end has a greater propensity to fray.

To test this hypothesis further, the strand-specific rates of cleavage of sense and anti-sense human *Cu, Zn superoxide dismutase-1* (*sod1*) RNA targets (Figure 3A) triggered by the siRNA duplex shown in Figure 3B were examined. Given that the 5′ ends of both siRNA strands of this duplex are in G:C base pairs, it was anticipated that this duplex would not display pronounced target cleavage asymmetry. As shown in Figure 3B, the two strands are similar in their rates of target cleavage, although the rate of anti-sense cleavage directed by the sense-strand is clearly faster than the rate of sense-target cleavage guided by the anti-sense strand. This small difference in rate is likely explained by the sense-strand forming 20 base pairs with its target RNA, whereas the

anti-sense strand can form only 19, consistent with previous reports that the penultimate position of an siRNA makes a small contribution to its efficacy (Elbashir et al., 2001b). Next, the C at position 19 of the sense strand was changed to A, causing the anti-sense strand to begin with an unpaired nucleotide. This change, which was made to the sense-strand of the siRNA, caused the rate of target cleavage guided by the *anti-sense* siRNA strand to be dramatically enhanced and the sense strand rate to be suppressed (Figure 3C). Because the enhancement of sense target cleavage was caused by a mutation in the sense siRNA strand, which does not participate in the recognition of the sense target, the effect of the mutation must be on a step in the RNAi pathway that is spatially or temporally coupled to siRNA unwinding. However, the suppression of anti-sense target cleavage clearly might have resulted from the single-nucleotie mismatch between the sense strand and its target RNA generated by the C-to-U substitution.

To test if the suppression of the rate of anti-sense target cleavage was a consequence of the position 19 mismatch, a different strategy was used to unpair the 5′ end of the anti-sense strand. Figure 3D shows an siRNA in which the sense-strand is identical to that in Figure 3B, but the first nucleotide of the anti-sense strand has been changed from G to U, creating a U-C mismatch at its 5′ end, in place of the G-A of Figure 3C. Nonetheless, this siRNA duplex showed pronounced asymmetry, with the anti-sense strand guiding target cleavage to the nearly complete exclusion of the sense strand (Figure 3D). Thus, the suppression of the cleavage rate of the sense-strand in Figure 3C was not a consequence of the position 19 mismatch. This finding is consistent with previous studies that suggest that mismatches with the target RNA are well tolerated if they occur near the 3′ end of the siRNA guide strand (Amarzguioui et al., 2003). The finding that the siRNAs in Figures 3C and 3D display profound asymmetry demonstrates that both the enhancement of the target cleavage rate of the anti-sense strand and the suppression of the function of the sense strand is a consequence of their relative abilities to enter the RNAi pathway, not their intrinsic capacity to direct target cleavage.

Finally, the sense strand of Figure 3C was paired with the anti-sense strand of Figure 3D to create the siRNA duplex shown in Figure 3E. The sense strand of this siRNA, like that in Figure 3C, contains a mismatch with the anti-sense target at position 19. Like the anti-sense siRNA strand in Figure 3D, the anti-sense strand contains a mismatch with the sense target at position 1. This siRNA duplex directs target anti-sense

cleavage significantly better than the siRNA in Figure 3C, despite the fact that the two siRNAs contain the same sense strand (Figure 3E).

Figures 3F, G, and H show a similar analysis in which the 5′ end of the sense strand or position 19 of the anti-sense strand of the siRNA in Figure 3B was altered to produce siRNA duplexes in which the 5′ end of the sense strand was either fully unpaired (Figures 3F and G) or paired in an A:U base pair (Figure 3H). Again, unpairing the 5′ end of an siRNA strand—the sense strand, in this case—caused that strand to function to the exclusion of the other strand. When the sense strand 5′ end was present in an A:U base pair and the anti-sense strand 5′ end was in a G:C pair, the sense strand dominated the reaction (Figure 3H), although now the anti-sense strand showed activity similar to that seen for the original siRNA (Figure 3B) in which both strands were in G:C pairs at their 5′ ends. Converting the unpaired 5′ end of the siRNAs in Figure 3 to an A:U pair reduced the functional asymmetry of the two strands by enhancing the efficacy of the sense strand (Figure 3E) or the anti-sense strand (Figure 3H). The relative ease with which the 5′ ends of the two siRNAs can be liberated from the duplex determines the degree of asymmetry. Additional data supporting this idea is shown in Figure 8, using a different siRNA. Figure 8B shows an siRNA that cleaved the two *sod1* target RNAs (Figure 8A). with modest functional asymmetry that reflects the collective base pairing strength of the first four or five nucleotides of each siRNA strand (Figure 8E; see below). Asymmetry was dramatically increased when a G:U wobble was introduced at the 5′ end of the anti-sense strand of the siRNA (Figure 8C), but no asymmetry was seen when the individual single-strands strands were used to trigger RNAi (Figure 8D), demonstrating that differential RISC assembly, not target accessibility, explains the functional asymmetry of the siRNA duplex.

Together, the data in Figures 1, 2, and 8 indicates that the symmetry of RISC assembly is determined by a competition between the fraying of the 5′ ends of the two siRNAs in the duplex. Such fraying may initiate a directional process of unwinding in which the strand at which unwinding is initiated preferentially enters RISC. Such a model requires that either that RISC assembly factors or RISC components themselves are loaded onto one of the two siRNA strands before unwinding is completed, or that information about the siRNA strands prior state of pairing is retained, perhaps by a protein such as the helicase remaining bound to a strand.

Example IV: A single hydrogen bond can determine which strand of an siRNA duplex directs RNAi

To explore this hypothesis further, additional changes were made to the *sod1*-specific siRNA in Figure 3. These modifications alter the function of the two strands of the siRNA, but do not change the site cleaved on the two target RNA's. In Figure 3A, the anti-sense strand of Figure 3B was paired with a sense strand identical to that in Figure 3B except the 5′ G was replace with inosine (I). Like G, I pairs with C, but makes two instead of three hydrogen bonds. In this respect, an I:C pair is similar in energy to an A:U pair. The resulting siRNA was functionally asymmetric, when the sense-strand began with an I, it directed tearget cleavage more efficiently than antisense-strand (Figure 4A). The asymmetry reflects an enhancement in efficacy of the sense siRNA strand, with little loss in the function of the anti-sense strand. An inosine at the 5′ end of the anti-sense strand had the opposite effect. When the G at position 1 of the anti-sense strand was substituted with inosine and the sense strand is that of Figure 3B, the anti-sense strand was enhanced relative to the sense strand (Figure 4B). Thus, the strand whose 5′ end is in the weaker base pair was more effective at target cleavage.

Remarkably, when the 5′ nucleotides of both siRNA strands engage in I:C base pairs (Figure 4C), the relative efficacy of the two siRNA strands is restored to that reported in Figure 3B. The slightly faster rate for anti-sense target cleavage than for sense target cleavage is also seen for RNAi triggered with the individual, inosine-containing single strands, indicating that it reflects a difference in the intrinsic capacity of the two strands to guide cleavage, rather than a difference in RISC assembly. Although the relative rates of cleavage of the two strands are comparable for the siRNAs in Figure 3B and 4C, the absolute rates are faster for the siRNA in Figure 4C. These data indicate that production of RISC from an individual strand is governed both by the relative propensity of the siRNA 5′ end to fray compared to that of its complementary strand and by the absolute propensity of the siRNA 5′ end to fray. This latter finding is particularly unexpected, in that it shows that a difference of a single hydrogen bond has a marked effect on the rate of RISC assembly. siRNA end fraying provides an entry site for an ATP-dependent RNA helicase that unwinds siRNA duplexes (Figure 4). The helicase makes many abortive attempts to dissociate the two siRNA strands before succeeding to load one strand into RISC. The involvement of a helicase in RISC assembly is supported by previous observations: (1) both siRNA unwinding and production of functional RISC

require ATP in vitro (Nykänen et al., 2001) and (2) several proteins with sequence homology to ATP-dependent RNA helicases have been implicated in RNA silencing (Wu-Scharf et al., 2000; Dalmay et al., 2001; Hutvágner and Zamore, 2002; Ishizuka et al., 2002; Kennerdell et al., 2002; Tabara et al., 2002; Tijsterman et al.,2002).

The effect of single-nucleotide mismatches in this region of the siRNA, using a series of siRNAs containing a mismatch at the second, third, or fourth position of each siRNA strand was further tested. The siRNAs bearing G:U wobble pairs at the second, third, or both second and third positions (Figure 11) was also analyzed. The results of this series demonstrate that mismatches, but not G:U wobbles, at positions 2-4 of an siRNA strand alter the relative loading of the two siRNA strands into RISC. Mismatches at position five, have very modest effects on the relative loading of the siRNA strands into RISC (data not shown). In contrast, the effects of internal mismatches at positions 6-15 cannot be explained by their influencing the symmetry of RISC assembly (data not shown). In sum, these data are consistent with the action of a non-processive helicase that can bind about four nucleotides of RNA.

Example V: Implications of siRNA asymmetry in miRNA biogenesis

One implication of the findings presented herein is that although siRNAs are predominantly present as duplexes at steady state *in vitro* (Nykänen et al., 2001) and perhaps *in vivo* (Hamilton and Baulcombe, 1999; Djikeng et al., 2001), both strands of an siRNA are unlikely to be present equally in RISC. That is, the strength of the base pairs at the 5′ ends of the two siRNA strands can influence their accumulation as single-strands. When the 5′ end of one strand is unpaired, this asymmetry can be nearly absolute. This observation suggested that asymmetric incorporation into RISC, as a consequence of directional unwinding from a frayed end of an siRNA duplex, might also explain why miRNAs accumulate as single strands. Animal miRNAs are derived from the double-stranded stem of ~ 70 nt stem-loop precursor RNAs (Lee et al., 1993; Pasquinelli et al., 2000; Reinhart et al., 2000; Lagos-Quintana et al., 2001; Lau et al., 2001; Lee and Ambros, 2001; Lagos-Quintana et al., 2002). pre-miRNAs stems are only partially double-stranded; the typical pre-miRNA contains mismatches, internal loops, and G•U base pairs predicted to distort an A-form RNA helix. miRNAs are generated from pre-miRNAs by the double-stranded RNA-specific endonuclease Dicer (Hutvágner et al., 2001; Grishok et al., 2001; Ketting et al., 2001). It was previously proposed by

the instant inventors that miRNAs are single-stranded because helical discontinuities constrain Dicer to break only two, rather than four, phosphodiester bonds, yielding a single-stranded miRNA, rather than an siRNA-like duplex (Hutvágner et al., 2001). Such a mechanism has precedent, because *E. coli* RNase III can be constrained by helical distortions to make only one or two breaks in an RNA chain (Chelladurai et al., 1993).

An alternative hypothesis is that the Dicer cleaves four phosphodiester bonds in all of its subtrates, both long dsRNA and pre-miRNAs, and always generates a product with the essential siRNA duplex (Hutvágner and Zamore, 2002; Reinhart et al., 2002; Lim et al., 2003b). This mechanism for miRNA production was originally suggested by Bartel and colleagues. Using a small RNA cloning strategy to identify mature miRNAs in *C. elegans*, they recovered small RNAs corresponding to the non-miRNA side of the precursor's stem (Lim et al., 2003b). Although these 'miRNA*' sequences were recovered at about 100 times lower frequency than the miRNAs themselves, they could always be paired with the corresponding miRNA to give 'miRNA duplexes' with 2 nt overhanging 3′ ends (Lim et al., 2003b). Their data suggest that miRNAs are born as duplexes, but accumulate as single-strands because some subsequent process stabilizes the miRNA, destabilizes the miRNA*, or both.

The incorporation of miRNA into RISC is this process. Our results with siRNA suggest that preferential assembly of a miRNA into the RISC would be accompanied by destruction of the miRNA. If the rate asymmetric RISC assembly was faster than the production of the miRNA duplexes, only single –stranded miRNAs would be observed at steady-state (Figure 4). The accumulation of single-strands and not duplexes for miRNAs would simply be a consequence of Dicer being significantly less efficient in cleaving pre-miRNAs compared to long dsRNA (Hutvágner et al., 2001). The rate of asymmetric RISC assembly might be faster than the production of miRNA duplexes, so only single-stranded miRNAs would be observed at steady-state. Two key predictions of this hypothesis are that (1) purified Dicer should cleave pre-miRNAs into equal amounts of miRNA and miRNA* products and (2) pre-miRNA structures should be processed by Dicer into duplexes with the 5′ end of the miRNA strand frayed or weakly hydrogen bonded and the 5′ end of the miRNA* strand more securely base paired.

A. Dicer cleaves pre-*let-7* symmetrically

To begin to test the idea that pre-miRNA are cleaved by Dicer to generate a product with an essential structure of an siRNA a duplex, we incubated the *Drosophila* pre-miRNA, pre-*let-7*, with purified, recombinant Dicer and analyzed the products by Northern hybridization using probes specific for either the 5′ side of the precursor stem that encodes mature *let-7* or for products derived from the 3′ side of the precursor stem (*let-7** products). As a control, the *let-7* precursor RNA was incubated in *Drosophila* embryo lysate, which recapitulates both pre-*let-7* maturation and RNAi *in vitro*. As previously reported, incubation of pre-*let-7* RNA in the lysate produced a single band corresponding to authentic *let-7*, but no *let-7** products (Hutvágner et al., 2001; Figure 5A and 5B). In contrast, incubation of pre-*let-7* with Dicer yielded approximately equal amounts of *let-7* and *let-7** products. At least three distinct RNAs were generated from each side of the stem, rather than the single band corresponding to mature *let-7* observed in the embryo lysate. Thus, the absence of *let-7** *in vivo* and in the embryo lysate reaction cannot be explained by the influence of pre-*let-7* structure on Dicer.

B. Asymmetric RISC assembly explains why miRNAs are single-stranded

If Dicer cleaves both sides of the pre-*let*-7 stem, then some step downstream from Dicer action selects mature *let-7* from an siRNA-like duplex in which *let-7* is paired with *let-7**. A good candidate for such a step would be the asymmetric incorporation of *let-7* into RISC, accompanied by the degradation of *let-7**. To test this idea, the siRNA that might be formed if pre-*let-7* were cleaved by Dicer into an siRNA duplex-like structure was deduced. The sequence of this 'pre-*let-7* siRNA,' generated by 'conceptual dicing,' is shown in Figure 6A (see below). Notably, the 5′ end of *let-7* is unpaired in this duplex, whereas the 5′ end of the *let-7** strand is in an A:U base pair. The results presented in Figures 2, 3, and 4 suggest that this structure should cause the *let-7* strand to enter the RISC to the near exclusion of the *let-7** strand, which would consequently be degraded.

C. miRNA versus miRNA* selection in *Drosophila*

This analysis was next extended to the other published *Drosophila* miRNA genes (Lagos-Quintana et al., 2001). For each precursor structure, the double-strand predicted to be produced by Dicer. These conceptually diced duplexes are shown in Figure 6A. For 23 of the 27 duplexes generated by this analysis (including pre-*let*-7), the difference in the base pairing of first five nucleotides of the miRNA versus miRNA* strands accurately predicted the miRNA, and not the miRNA,* accumulates *in vivo*. The analysis succeeded irrespective of which side of the pre-miRNA stem encoded the mature miRNA. This analysis, previous observations that single mismatches in the first four nucleotides of an siRNA strand, an initial G:U wobble pair, but not internal G:U wobbles, directed the asymmetric incorporation of an siRNA strand into RISC (Figures 1, 2, 3, 8, 9, and 11). However, no difference was discerned in the propensity to fray of the 5′ ends of the miRNA and * strands for miR-4, miR-5, the three miR-6-2 paralogs, and miR-10. Therefore, it could not be explained why a particular strand would accumulate as the mature miRNA for these three miRNA precursors. miR-5 and miR-10, like other *Drosophila* miRNAs, were identified by the cloning and sequencing of small RNAs from embryos (Lagos-Quintana et al., 2001). Determinants other than end fraying appear to function in the selection of miR-4 and miR-6; these unknown determinants may also play a role in the assembly of an siRNA atrand into RISC. However, miR-5 and miR-10 were cloned only once, raising the possibility that miR-5* or miR-10* is present in embryos, but not represented among the library of small RNA's from which the miRNAs were cloned. Similarly, miR-6 is encoded by three paralogous genes, only one of which we predict to produce detectable amounts of the miR*, so this * strand might have also gone undetected. To test if both the miRNA and * strands might accumulate for some or all of these three genes, Northern hybridization was used to examined the relative abundance of miR-10 and miR-10* in adult *Drosophila* males and females, and in syncitial blastoderm embryos. The results detected both miR-10* and mi-R10 *in vivo* (Figure 6C). In fact, the results indicated that more miR-10* was detected that miR-10 in adult males. This finding strengthens the proposal that miRNA genes (*i.e.*, premiRNA's) uniquely specify on which side of the stem the miRNA residues by generating siRNA-like duplexes from which only one of the two strands of the duplex is assembled into RISC. When these double-stranded intermediates do not contain structural features enforcing asymmetric RISC assembly, both strands

accumulate *in vivo*. It is possible that pre-miRNAs such as pre-miR-10, which generates roughly equal amounts of small RNA products from both sides of the precursor stem, simultaneously regulate target RNAs with partial complementary to both small RNA products.

Example VI: Increased rate of siRNA efficency through the use of dTdT tails

Art-recognized protocols for designing siRNA duplexes teach the inclusion of dTdT tails (*i.e.*, 2-nucleotide overhangs consisting of dTs). Two duplexes were created to test whether the addition of 3'overhanging dTdT tails increases the rate of siRNA taegeting efficiency of the *Cu, Zn superoxide-dismutase-1 (Sod1)* mRNA. The first duplex contained sense and antisense stands, each including 21 nucleotides with 19 complementary bases plus 2-nucleotide overhangs (the overhangs onsisting of bases in common with the target sequence). The second duplex contained sense and antisense strands, each including 19 complementary nucleotides (in common with the *Sod1* target), plus 2-nucleotide dTdT tails at the 5' end of the strand (not matching the *Sod1* target). Results demonstrate that the rate of siRNA efficiency improved ~ 8 fold ~ when using the duplex having mismatched dTdT tails (Figure 12).

Discussion of Examples I-VI: Implications for RNA silencing

The observations described herein provide rules for siRNA design. Clearly, siRNA structure can profoundly influence the entry of the anti-sense siRNA strand into the RNAi pathway. Thus, the sequence of the siRNA, rather than that of the target site, may explain at least some previous reports of ineffective siRNAs duplexes. Such inactive duplexes may be coaxed back to life by modifying the sense strand of the siRNA to reduce the strength of the base pair at the 5′ end of the anti-sense strand. An example of this *in vitro* is shown in Figure 9, for an ineffective siRNA directed against the *huntingtin (htt)* mRNA (Figure 9A). Changing the G:C (Figure 9B) to an A:U pair (Figure 9C) or a G-A mismatch (Figure 9D) dramatically improved its target cleavage rate in vitro and its efficacy *in vivo* (Eftim Milkani, NA, and PDZ, unpublished observations). In fact, Khvorova and colleagues have found that a low base-pairing stability at the 5′ end of the antisense strand, but not the sense strand, is a prerequisite

for siRNA function in cultured mammalian cells (Anastasia Khvorova, Angela Reynolds, and Sumedha D. Jayasena, manuscript submitted).

siRNAs designed to function asymmetrically may also be uses to enhance RNAi specificity. Recently, expression profiling studies have shown that the sense-strand of an siRNA can direct off-target gene silencing (A.L. Jackson, et al. (2003) *Nature Biotechnology*, May 18). The data presented herein provide a strategy for eliminating such sequence-specific but undesirable effects: redesigning the siRNA so that only the anti-sense strand enters the RNAi pathway.

The observations described herein provide new design rules for the construction of short hairpin RNAs (shRNAs), which produce siRNAs transcriptionally in cultured cells or *in vivo* (Brummelkamp et al., 2002; McManus et al., 2002; Paddison et al., 2002; Paul et al., 2002; Sui et al., 2002; Yu et al., 2002). shRNA strategies typically employ a *Pol* III promoter to drive transcription, so the shRNA must begin with several G residues. As a consequence, the 5′ end of the siRNA may be sequestered in a G:C base pair, significantly reducing entry of the anti-sense strand into the RNAi pathway. To avoid this problem, the anti-sense strand of the desired siRNA can be placed on the 3′ side of the loop, so as to ensure that its 5′ end is in an A:U, rather than the G:C pair typically encoded. Alternatively, the hairpin can be designed to place the 5′ end of the anti-sense siRNA strand in a mismatch or G•U base pair, in which case it can be placed on either side of the stem. Moreover, a recent report suggests that some shRNAs may induce the interferon response (Bridge et al., 2003). The data suggest that mismatches and G:U pairs could be designed into these shRNAs simultaneously to promote entry of the correct siRNA strand into the RNAi pathway and to diminish the capacity of the shRNA stem to trigger non-sequence specific responses to double-stranded RNA.

Finally, the data identify an unanticipated step in the RNAi pathway: the direct coupling of siRNA unwinding to RISC assembly. This finding suggests that the helicase responsible for unwinding siRNA duplexes will be intimately linked to other components of the RNAi machinery. Identifying the helicase and the proteins with which it functions to assemble the RISC is clearly an important challenge for the future.

Example VII: The siRNA-programmed RISC is an enzyme

RISC programmed with small RNA in vivo catalyzes the destruction of target RNA in vitro without consuming its small RNA guide (Tang et al., 2003) (Hutvàgner et al., 2002). To begin a kinetic analysis of RISC, the RISC programmed in vitro with siRNA is likewise a multiple-turnover enzyme was first confirmed. To engineer an RNAi reaction that contained a high substrate concentration relative to RISC, an siRNA was used in which the guide strand is identical to the let-7 miRNA, but unlike the miRNA, the let-7 siRNA is paired to an RNA strand anti-sense to let-7(Hutvàgner et al., 2002). The let-7 strand of this siRNA has a high intrinsic cleaving activity, but a reduced efficiency of incorporation into RISC (Figure 19A).

After incubating the let-7 siRNA with Drosophila embryo lysate in the presence of ATP, RISC assembly was inactivated by treatment with N-ethyl maleimide (NEM), and the amount of RISC generated was measured using the previously described tethered 2′-O-methyl oligonucleotide assay (Hutvagner et al., 2004; Schwartz et al., 2003) (Figure 19 B,C). The amount of let-7 programmed RISC increased with increasing siRNA concentration, until the assembly reaction began to saturate at ~50 nM, reaching an asymptote between 3 and 4 nM RISC. Using 0.6 nM RISC, >50 cycles of target recognition and cleavage per enzyme complex (data not shown) was observed, confirming that siRNA-programmed RISC is a multiple-turnover enzyme.

Example VIII: Multiple-turnover is limited by product release

The evaluation of the kinetics of siRNA-directed target cleavage in the presence or absence of ATP was further performed (Figure 13). RISC was assembled in the presence of ATP, then the energy regenerating enzyme, creatine kinase, was inactivated with NEM, and ATP depleted by adding hexokinase and glucose (–ATP conditions). For +ATP measurements creatine kinase was added to the reaction after NEM-treatment, and the hexokinase treatment was omitted. A faster rate of cleavage in the presence than in the absence of ATP was observed. This difference was only apparent late in the reaction time course, indiciating that the ATP-dependent rate of cleavage was faster than the ATP-independent rate only at steady state (Figure 13 A). The analysis was repeated in more detail (Figure 13 B). In the absence of ATP, a burst of cleaved product early in the reaction, followed by a ~4-fold slower rate of target cleavage was observed. No burst was observed in the presence of ATP (Figure 13A). If the burst corresponds to a single-

turnover of enzyme, then extrapolation of the slower steady state rate back to the y-axis should give the amount of active enzyme in the reaction. The y-intercept at the start of the reaction for the steady-state rate was 4.9 nM, in good agreement with the amount of RISC estimated using the tethered 2′-O-methyl oligonucleotide assay (~4 nM; Figure 13 B).

In principle, ATP could enhance target recognition by RISC, promote a rearrangement of the RISC/target complex to an active form, facilitate cleavage itself, promote the release of the cleavage products from the siRNA guide strand, or help restore RISC to a catalytically competent state after product release. All of these steps, except product release and restoration to catalytic competence, should affect the rate of both multiple and single-turnover reactions. Therefore, the rate of reaction in the presence and in the absence of ATP under conditions in which RISC was in excess over the RNA target was analyzed. At early times under these conditions, the reaction rate should reflect only single-turnover cleavage events, in which events after cleavage do not determine the rate of reaction. Using single-turnover reaction conditions, identical rates of RISC-mediated cleavage in the presence or absence of ATP was observed (Figure 13 C). Thus, ATP must enhance a step that occurs only when each RISC catalyzes multiple cycles of target cleavage.

If product release is rate-determining for multiple-turnover catalysis by RISC in the absence, but not the presence, of ATP, then modifications that weaken the strength of pairing to the target RNA might enhance product release, but would not be expected to accelerate the return of the RISC to a catalytically competent state. Mismatches between the siRNA and its RNA target at the 3′ end of the siRNA guide strand was incorporated and designed the siRNAs to be functionally asymmetric, ensuring efficient and

predictable incorporation of the let-7 strand into RISC (Figure 14 A). The reaction velocity under conditions of substrate excess in the presence and in the absence of ATP for siRNAs with zero to four mismatches between the guide strand 3′ end and the RNA target were compared. Cleavage was measured from 100 and 540 s, when > 90% of the target remained uncleaved, ensuring that the multiple-turnover reaction was at steady state. Even a single 3′ mismatch between the siRNA and its target increased the –ATP rate, relative to the +ATP rate, and siRNAs with two or more mismatches showed no significant difference in rate between the presence and absence of ATP (Figure 14B).

The results indicated that in the absence of ATP, product release is the rate-determining step for siRNAs fully matched to their RNA targets.

Example IX: siRNA:target complementarity and RISC function

Mismatches between the siRNA and its target facilitate product release, but not without cost: the rate of reaction, irrespective of ATP concentration, decreases with each additional 3′ mismatch. When the concentration of RISC was ~16–80-fold greater than the target RNA concentration, each additional mismatch between the 3′ end of the siRNA guide strand and the RNA target further slowed the reaction (Figure 14 C,D). Under conditions of substrate excess, the effect of mismatches between the 3′ end of the siRNA guide strand and its RNA target was more striking (Figure 15A): the rate of cleavage slowed ~20% for each additional mismatch. To test the limits of the tolerance of RISC for 3′ mismatches, cleavage under modest (8-fold, Figure 15 B) and vast (~80-fold, Figure 15 C and 16 C) enzyme excess over target RNA was analyzed. Remarkably, cleavage was detected for siRNAs with as many as nine 3′ mismatches to the RNA target (Figure 15 C and 16 C), but only after 24 hour incubation. No cleavage was detected for an siRNA with ten 3′ mismatches to the RNA target (Figure 15 C).

Linsley and colleagues have proposed siRNA-directed down-regulation of an mRNA with as few as eleven contiguous bases complementary to the siRNA guide strand (Jackson et al., 2003). In that study, the mRNA target paired with both nts 2–5 and nts 7–17 of the siRNA guide strand, but mismatched at nts 1 and 6 of the siRNA. Results indicated that up to five mismatched bases are tolerated between the 5′ end of the siRNA and its RNA target (Figure 16 A,B). No cleavage was detected for siRNAs with six, seven, or eight 5′ mismatches to the target, even after 24 hour incubation. The siRNA bearing eight mismatches between its 5′ end and the let-7 complementary target was fully active when eight compensatory mutations were introduced into the let-7 binding site (Figure 15C and 16B), demonstrating that mutation of the siRNA was not the cause for its inactivity against the mismatched target. Similarly, when eight mismatches with the 3′ or 5′ end of the siRNA were created by changing the sequence of the RNA target, target RNA cleavage when the target contained eight mismatches with the siRNA 3′ end, but not with the 5′ end was detected (Figure16 B,C).

To begin to estimate the minimal number of base pairs between the siRNA and its target that permit detectable cleavage by RISC at 24 hour incubation, seven, eight, or nine 3′ mismatches with increasing numbers of 5′ mismatches were combined (Figure 16 C). Cleavage was detected for as many as nine 3′ mismatches. However, no detectable cleavage occurred when seven, eight, or nine 3′ mismatches were combined with two or more 5′ mismatches. In contrast, a single 5′ mismatch (p1) enhanced target cleavage directed by all three 3′mismatched siRNAs. Only 6% of the target RNA was cleaved after 24 hours when the siRNA contained nine contiguous 3′ mismatches with the target RNA, but 10% was cleaved when the siRNA contained both nine 3′ mismatches and a single (p1) 5′ mismatch. Cleavage was similarly enhanced by the addition of a p1 mismatch to seven 3′ mismatches (49% cleavage versus 75% cleavage at 24 hours) or to eight 3′ mismatches (21% versus 42% cleavage at 24 hours). The finding that unpairing of the first base of the siRNA guide strand potentiated cleavage under single-turnover conditions inducated that a conformational change occurs in RISC during which the paired p1 base becomes unpaired prior to cleavage. Intriguingly, p1 is often predicted to be unpaired for miRNAs bound to their targets (Lewis et al., 2003; Rhoades et al., 2002; Stark et al., 2003).

For siRNAs that pair fully with their RNA targets, the scissile phosphate always lies between the target nucleotides that pair with siRNA bases 10 and 11 (Elbashir et al., 2001; Elbashir et al., 2001). Analysis at single nucleotide resolution of the 5′ cleavage products generated by siRNAs with three, four, or five 5′ mismatches (Figure 16 D) or six 3′ terminal mismatches (data not shown) revealed that the scissile phosphate on the target RNA remained the same, even when five 5′ nts of the siRNA guide strand were mismatched with the target RNA (Figure 16 D). As discussed below, this result indicates that the identity of the scissile phosphate is a consequence of the structure of RISC, rather than being measured from the 5′ end of the helix formed between the siRNA and its RNA target.

Example X: Kinetic analysis of RISC catalysis

The role of nucleotides in the terminal regions of the siRNA guide strand in directing RISC activitywas next studied. Reduced pairing between an siRNA and its target might disrupt the binding of RISC to its target. Alternatively, mismatches might disrupt the structure, but not the affinity, of the siRNA/target interaction. Fully matched

siRNAs are thought to form a 21 base-pair, A-form helix with the target RNA (Chiu et al., 2003; Shiu et al., 2002), but do all parts of this helix contribute equally to target binding or do some regions provide only a catalytically permissive geometry? To distinguish between these possibilities, the Michaelis-Menten kinetics of siRNA-directed target-RNA cleavage for a perfectly matched siRNA and for three siRNAs mismatched at their termini was analyzed. siRNAs were assembled into RISC, then diluted with reaction buffer to the desired RISC concentration and mixed with target RNA. For each siRNA, the initial velocity of reaction was determined at multiple substrate concentrations (Figure 21 A), and KM and kcat determined from a non-linear least squares fit of substrate concentration versus initial velocity (Figure 17 A). By this assay, the KM of the let-7 siRNA with complete complementarity to its target was ~8.4 nM was estimated (Table 1). A significant difference in KM, within error, between the fully paired siRNA and siRNA variants bearing three to five mismatches at their 3′ end or three mismatches at their 5′ end was not detected (Figure 17A and Table 1). For the mismatched siRNAs a higher than optimal enzyme concentration in order to detect cleavage was used. Therefore, the KM measurements for the mismatched siRNAs represent an upper bound for the actual KM values.

While the KM was unaltered for the let-7 siRNA containing several terminal mismatches, the turnover number, kcat, was decreased by terminal mismatches (Table 1). Three mismatches at either the 3′ or the 5′ end of the siRNA halved the kcat. The introduction of five, 3′ mismatches also had no significant effect on KM, yet decreased kcat nearly 17-fold (Table 1).

Table 1 Summarizes the kinetic data from the analysis in Figure 17A. For comparison, the KM and kcat values of four well studied protein enzymes are provided. KM and kcat ± error of fit are reported.

Example XI: KM reflects the binding strength of RISC

To estimate the contribution of binding to KM, a competition assay that measures the ability of 2′-O-methyl oligonucleotides to inhibit target cleavage by RISC was used (Figure 17 B,C). Such a strategy was used previously to analyze the mechanism of target destruction by antisense oligonucleotides that recruit RNase H (Lima et al., 1997). The anticipation was that 2′-O-methyl oligonucleotides would act as

competitive inhibitors of RISC, because they bind to RISC containing complementary siRNA but not to RISC containing unrelated siRNA (Hutvàgner et al., 2004; Meister et al., 2004). Thirty-one nt long, 2′-O-methyl oligonucleotides were designed as described previously (Hutvàgner et al., 2004), taking care to exclude sequences predicted to form stable internal structures. 2′-O-methyl oligonucleotides were chosen because of their marked stability in Drosophila lysate and because they can be added to the reaction at high μM concentration.

Competition by 2′-O-methyl oligonucleotides and bona fide RNA targets was quantitatively similar. The reaction velocities of siRNA-directed cleavage of a 32P-radiolabled target in the presence of increasing concentrations of unlabeled capped RNA target or a 31-nt 2′-O-methyl oligonucleotide corresponding to the region of the target containing the siRNA binding site was analyzed (Figure 17 B). Lineweaver-Burk analysis of the data confirm that 2′-O-methyl oligonucleotides act as competitive inhibitors of RISC (data not shown). These data were used to calculate Ki values for the perfectly matched RNA and 2′-O-methyl competitors. For the capped RNA competitor, the Ki was ~7.7 ± 4 nM (Figure 17 B), nearly identical to the KM for this siRNA, 8.4 nM (Table 1). The Ki for the perfectly matched 2′-O-methyl competitor oligonucleotide was 3.2 ± 1 nM (Figure 17 B), essentially the same, within error, as that of the all-RNA competitor. The results indicated that 2′-O-methyl oligonucleotides are good models for 5′-capped RNA targets and that the KM for target cleavage by RISC is largely determined by the affinity (KD) of RISC for its target RNA.

Although targets with more than five contiguous mismatches to either end of the siRNA are poor substrates for cleavage, they might nonetheless bind RISC and compete with the 32P-radiolabeled target RNA. The 2′-O-methyl oligonucleotide competition assay to determine the Ki values for oligonucleotides containing as many as eight mismatches to the siRNA guide strand was used (Figure 17 B). 2′-O-methyl oligonucleotides with 3′ terminal mismatches to the siRNA were good competitors: a four nucleotide mismatch with the 3′ end of the siRNA increased the Ki by only ~3-fold (9.0 ± 0.9 nM) and an eight nucleotide mismatch with the 3′ end of the siRNA increased the Ki by ~10-fold (34.8 ± 7 nM). In contrast, mismatches with the 5′ end of the siRNA had a dramatic effect on binding. A four nucleotide mismatch to the 5′ end of the siRNA increased the Ki ~12-fold (36.4 ± 9.2 nM) and an eight nucleotide mismatch to the 5′ end of the siRNA increased the Ki 53-fold (173 ± 16 nM). The differential effect on

binding between 5′ and 3′ mismatches was maintained even at the center of the siRNA: a 2′-O-methyl oligonucleotide bearing four mismatches with siRNA nucleotides 11, 12, 13, and 14 (4 nt 3′ central mismatch, Figure 17 B) bound more tightly to RISC (*i.e.*, had a lower Ki) than an oligonucleotide with four mismatches to siRNA positions 7, 8, 9, and 10 (4 nt 5′ central mismatch, Figure 17 B).

Discussion of Examples VII-XI:

RISC programmed with exogenous siRNA is an enzyme, capable of multiple rounds of target cleavage. Prevoius studies showed that cleavage of a target RNA by RISC does not require ATP (Nykänen et al., 2001; Tomari et al., 2004). The more detailed kinetic analysis presented herein indicates that there are no ATP-assisted steps in either target recognition or cleavage by Drosophila RISC; no difference in rate in the presence or absence of ATP for RNAi reactions analyzed under conditions of substrate excess at early time points (pre-steady state) or under conditions of enzyme excess where the reaction was essentially single-turnover was detected. In contrast, the steady-state rate of cleavage under multiple turnover conditions was enhanced four-fold by ATP. The results indicates that release of the products of the RISC endonuclease is rate determining under these conditions in the absence of ATP, but not in the presence of ATP. The most straightforward explanation for this finding is that an ATP-dependent RNA helicase facilitates the dissociation of the products of target cleavage from the RISC-bound siRNA. The involvement of such an ATP-dependent helicase in RNAi *in vivo* may explain why siRNAs can be active within a broad range of GC content (Reynolds et al., 2004).

In the presence of ATP, siRNA-programmed Drosophila RISC is a classical Michaelis-Menten enzyme. The guide strand of the siRNA studied here has the sequence of let-7, an endogenous miRNA. *In vivo*, let-7 is not thought to direct mRNA cleavage, but rather is believed to repress productive translation of its mRNA targets. Nonetheless, the let-7 siRNA is among the most potent of the siRNAs we have studied *in vitro* and provides a good model for effective siRNA in general. With a kcat of ~7 x 10–3 s–1, the let-7 siRNA-programmed RISC was slow compared to enzymes with small molecule substrates (Table 1). The KM for this RISC was ~8 nM. Enzymes typically have KM values between 1- and 100-fold greater than the physiological concentrations of their substrates (Stryer et al., 1981). The results indicate that RISC is no exception: individual

abundant mRNA species are present in eukaryotic cells at high pM or low nM concentration. The KM of RISC is likely determined primarily by the strength of its interaction with the target RNA, because the KM is nearly identical to the Ki of a non-cleavable 2′-O-methyl oligonucleotide inhibitor.

Recently, a study of the kinetic parameters of target RNA cleavage by human RISC was described (Martinez et al., 2004). In that study, the minimal active human RISC was highly purified; in this study, Drosophila RISC activity was measured for the unpurified, intact holo-RISC, believed to be an 80S multi-protein complex (Pham et al., 2004). Different siRNAs were used in the two studies. Nonetheless, the KM and kcat values reported here and for the minimal human RISC are remarkably similar: the KM was 2.7–8.4 nM and the kcat was 7.1 x 10-3 sec-1 for the let-7 siRNA-programmed Drosophila holo-RISC versus a KM of 1.1–2.3 nM and a kcat of 1.7 x 10-2 sec-1 for a different siRNA in minimal human RISC. As in this study, a pre-steady-state burst was observed in the absence of ATP, consistent with the idea that product release is ATP-assisted in vivo.

The ratio of kcat to KM is a classical measure of enzyme efficiency and corresponds to the second order rate constant for the reaction when the concentration of substrate is much less than the KM. For the let-7 programmed RISC, kcat KM–1 equals ~8.4 x 105 M–1 –1 (~8.4 x 10–4 nM–1 s–1), a value far slower than the expected rate of collision of RISC –1 with mRNA, =107 M–1 s. It is possible that the rate of catalysis by RISC is constrained by the rate of conformational changes required for formation of the enzyme-substrate complex or by subsequent conformational rearrangements required for catalysis. It is possible that siRNAs can be designed that significantly improve either the kcat or KM of RISC without compromising specificity.

Although siRNAs are typically envisioned to bind their target RNAs through 19 to 21 complementary base pairs, we find that the 5′, central, and 3′ regions of the siRNA make distinct contributions to binding and catalysis (Figure 18). Measurements of KM and Ki suggest that the 5′ nucleotides of the siRNA contribute more to target binding than do the 3′ nucleotides. At least for the siRNA examined here, the first three and the last five nucleotides of a 21 nt siRNA contribute little to binding. If the KD of RISC bound to its target RNA is essentially its KM, ~8 nM, then the free energy (.G° = –RT lin KD) of the let-7-programmed RISC:target interaction is approximately –11 kcal mol–1, considerably less than the –35 kcal mol–1 (KD ~10–29) predicted32 for the let-7

RNA bound to a fully complementary RNA in 100 mM K+ and 1.2 mM Mg2+ at 25°C. It is possible that RISC discards potential binding energy by binding less tightly to its target, an siRNA in RISC gains the ability to discriminate between well matched and poorly match targets, but only for bases in the 5′ region of the siRNA guide strand.

Mismatches between the central and 3′ regions of an siRNA and its target RNA reduce kcat far more than mismatches at the 5′ end of the siRNA. These results fit well with recent findings by Doench and Sharp that translational repression by siRNA, designed to act like animal miRNA, is dramatically disrupted by mismatches with the 5′ end of the siRNA, but not with similar mismatches at the 3′ end18. These authors propose that miRNA binding is mediated primarily by nucleotides at the 5′ end of the small RNA. In fact, complementarity between the 5′ end of miRNAs and their targets has been required by all computational approaches for predicting animal miRNA targets (Rajewsky et al., 2004; Lewis et al., 2003; Stark et al., 2003; Enright et al., 2003). The instant discovery that central and 3′ siRNA sequences must pair with the target sequence for effective target cleavage but not for target binding reinforces this view; both central and 3′ miRNA sequences are usually mismatched with their binding sites in their natural targets (Lee et al., 1993; Reinhart et al., 2000; Brennecke et al., 2003; Abrahante et al., 2003; Vella et al., 2004; Xu et al., 2003; Johnston et al., 2003).

Formation of a contiguous A-form helix surrounding the scissile phosphate of the target mRNA has been proposed to be a quality control step for RISC-mediated target cleavage (Chiu et al., 2003). The instant invention discovers that RISC can direct cleavage when the siRNA is paired with the target RNA only at nts 2–12 of the guide strand, corresponding to one complete turn of an RNA:RNA helix. This region of the siRNA includes nts 2–8, which appear to be critical for miRNA recognition of mRNAs targeted for translational repression, plus two nts flanking either side of the scissile phosphate. The instant invention further discovers unpairing the first nt of the guide strand enhances the activity of siRNAs with seven, eight or nine 3′ mismatches to the RNA target is striking, since many miRNAs do not pair with their targets at this position. Furthermore, such pairing resembles that reported by Linsley and colleagues for siRNA-directed off-target effects in cultured mammalian cells (Jackson et al., 2003).

The requirement for a full turn of a helix may reflect a mechanism of 'quality control' by RISC. Since RISC can apparently assemble on any siRNA sequence, it must use the structure of the siRNA paired to its target to determine whether or not to cleave.

Despite the apparent surveillance of the structure of the siRNA/target pair, the identity of the scissile phosphate is unaltered by extensive mismatch between the 5′ end of the siRNA and its target. Yet the scissile phosphate is determined by its distance from the 5′ end of the siRNA guide strand (Elbashir et al., 2001; Elbashir et al., 2001). The simplest explanation for the instant discovery is that the scissile phosphate is identified by a protein loaded onto the siRNA during RISC assembly, *i.e.,* before the encounter of the RISC with its target RNA.

The remarkable tolerance of RISC for mismatches between the siRNA and its targets—up to nine contiguous 3′ nucleotides—implies that a large number off-target genes should be expected for many siRNA sequences when RISC is present in excess over its RNA targets. However, RISC with extensive mismatches between the siRNA and target are quite slow to cleave, so off-target effects may be minimized by keeping the amount of RISC as low as possible. These understandings of the molecular basis of siRNA-directed gene silencing assist the skilled artisan in creating siRNAs designed to balance the competing demands of siRNA efficacy and specificity.

Experimental Procedures

A. General methods

Drosophila embryo lysate preparation, *in vitro* RNAi reactions, and cap-labeling of target RNAs using Guanylyl transferase were carried out as previously described (Tuschl et al., 1999; Zamore et al., 2000). Target RNAs were used at ~ 5 nM concentration to ensure that reactions occurred under single-turnover conditions. Target cleavage under these conditions was proportionate to siRNA concentrations. Cleavage products of RNAi reactions were analyzed by electrophoresis on 5% or 8% denaturing acrylamide gels. 5′ end labeling and determination of siRNA unwinding status were according to Nykänen et al. (Nykänen et al., 2001) except that unlabeled competitor RNA was used at 100-fold molar excess. Gels were dried, then exposed to image plates (Fuji), which were scanned with a Fuji FLA-5000 phosphorimager. Images were analyzed using Image Reader FLA-5000 version 1.0 (Fuji) and Image Gauge version 3.45 or 4.1 (Fuji). Data analysis was performed using Excel (Microsoft) and IgorPro 5.0 (Wavemetrics).

B. Drosophila embryo lysate, siRNA labeling with polynucleotide kinase (New England Biolabs), target RNA preparation and labeling with guanylyl transferase were carried out as described (Hutvàgner et al., 2002, Haley et al., 2003) and the forward primer sequence for 379 nt target mRNA was 5′-CGC TAA TAC GAC TCA CTA TAG CAG TTG GCG CCG CGA ACG A-3′, and 5′-GCG TAA TAC GAC TCA CTA TAG TCA CAT CTC ATC TAC CTC C-3 for the 182 nt target. Reverse primers used to generate fully matched and mismatched target RNAs were: 5′-CCC ATT TAG GTG ACA CTA TAG ATT TAC ATC GCG TTG AGT GTA GAA CGG TTG TAT AAA AGG TTG AGG TAG TAG GTT GTA TAG TGA AGA GAG GAG TTC ATG ATC AGT G-3′ (perfect match to let-7); 5′-CCC ATT TAG GTG ACA CTA TAG ATT TAC ATC GCG TTG AGT GTA GAA CGG TTG TAT AAA AGG TTG AGG TAG TAG GTT CAT GCA GGA AGA GAG GAG TTC ATG ATC AGT G-3′(7 nt 3′ mismatch); 5′-CCC ATT TAG GTG ACA CTA TAG ATT TAC ATC GCG TTG AGT GTA GAA CGG TTG TAT AAA AGG TTG AGG TAG TAG GTA CAU GCA GGA AGA GAG GAG TTC ATG ATC AGT G-3′ (8 nt 3′ mismatch); 5′-CCC ATT TAG GTG ACA CTA TAG ATT TAC ATC GCG TTG AGT GTA GAA CGG TTG TAT AAA AGG TTG AGG TAG TAG GAA CAT GCA GGA AGA GAG GAG TTC ATG ATC AGT G-3′ (9 nt 3′ mismatch); 5′-CCC ATT TAG GTG ACA CTA TAG ATT TAC ATC GCG TTG AGT GTA GAA CGG TTG TAT AAA AGG TAC TCC ATC TAG GTT GTA TAG TGA AGA GAG GAG TTC ATG ATC AGT G-3′(8 nt 5′mismatch); 5′-CCC ATT TAG GTG ACA CTA TAG ATT TAC ATC GCG TTG AGT GTA GAA CGG TTG TAT AAA AGG TAC TCG TAG TAG GTT GTA TAG TGA AGA GAG GAG TTC ATG ATC AGT G-3′ (4 nt 5′mismatch). In Figures 13, 14, 15, 17A, 19 and 20A, the target sequence was 613 nt long; 379 nt in Figures 16A-C,17B and 20B; and 182 nt in Figure 16D. All siRNAs were deprotected according to the manufacturer's protocol (Dharmacon), 5′-radiolabeled where appropriate, then gel purified on a 15% denaturing polyacrylamide gel. 2′-O-methyl oligonucleotides were from Dharmacon. siRNA strands were annealed at high concentrations and serially diluted into lysis buffer (30 nM HEPES pH 7.4, 100 mM KOAc, and 2 mM MgCl2). Gels were dried and imaged as described (Schwartz et al., 2003). Images were analyzed using Image Gauge 4.1 (Fuji). Initial rates were determined by linear regression using Excel X (Microsoft) or IgorPro 5.01 (Wavemetrics). Kaleidagraph 3.6.2 (Synergy Software) was used to determine KM and Ki by global fitting to the equations: V = (Vmax xS)(KM + S)–1 and

V = (Vmax xKi(app))(Ki(app) + I)–1, where V is velocity, S is target RNA concentration, and I is the concentration of 2′-O-methyl oligonucleotide competitor. Ki was calculated by correcting Ki(app) by the KM and substrate concentration, Ki = Ki(app)(1+(S KM–1))–1.

C. siRNA preparation

Synthetic RNAs (Dharmacon) were deprotected according to the manufacturer's protocol. siRNA strands were annealed (Elbashir et al., 2001a) and used at 50 nM final concentration unless otherwise noted. siRNA single strands were phosphorylated with polynucleotide kinase (New England Biolabs) and 1 mM ATP according to the manufacturer's directions and used at 500 nM final concentration.

D. Target RNA preparation

Target RNAs were transcribed with recombinant, histidine-tagged, T7 RNA Polymerase from PCR products as described (Nykänen et al., 2001; Hutvágner and Zamore, 2002), except for sense *sod1* mRNA, which was transcribed from a plasmid template (Crow et al., 1997) linearized with Bam HI. PCR templates for *htt* sense and anti-sense and *sod1* anti-sense target RNAs were generated by amplifying 0.1 ng/ml (final concentration) plasmid template encoding *htt* or *sod1* cDNA using the following primer pairs: *htt* sense target, 5′-GCG TAA TAC GAC TCA CTA TAG GAA CAG TAT GTC TCA GAC ATC-3′ and 5′-UUCG AAG UAU UCC GCG UAC GU-3′; *htt* anti-sense target, 5′-GCG TAA TAC GAC TCA CTA TAG GAC AAG CCT AAT TAG TGATGC-3′ and 5′-GAA CAG TAT GTC TCA GAC ATC-3′; *sod1* anti-sense target, 5′-GCG TAA TAC GAC TCA CTA TAG GGC TTT GTT AGC AGC CGG AT-3′ and 5′-GGG AGA CCA CAA CGG TTT CCC-3′.

Immobilized 2′-O-methyl oligonucleotide capture of RISC

The 5′ end of the siRNA strand to be measured was 32 P-radiolabeled with PNK. 10 pmol biotinylated 2′-O-Methyl RNA was immobilized on Dynabeads M280 (Dynal) by incubation in 10 ml lysis buffer containing 2mM DTT for 1 h on ice with the equivalent of 50 ml of the suspension of beads provided by the manufacturer. The beads were then washed to remove unbound oligonucleotide. 50 nM siRNA was pre-incubated

in a standard 50 ml in vitro RNAi reaction for 15 min at 25°*C*. Then, all of the immobilized 2′-O-Methyl oligonucleotide was added to the reaction and the incubation continued for 1 h at 25°C. After incubation, the beads were rapidly washed three times with lysis buffer containing 0.1% (w/v) NP-40 and 2 mM DTT followed by a wash with the same buffer without NP-40. Input and bound radioactivity were determined by scintillation counting (Beckman). The 5′-biotin moiety was linked via a six-carbon spacer arm. 2′-O-methyl oligonucleotides (IDT) were: 5′-biotin-ACA UUU CGA AGU AUU CCG CGU ACG UGA UGU U-3′ (to capture the siRNA sense strand) 5′-biotin-CAU CAC GUA CGC GGA AUA CUU CGA AAU GUC C-3′ (to capture the anti-sense strand).

mfold Analysis

To model the end of an siRNA, the following 16 nt RNA sequence were submitted to mfold 3.1: (37°C, 1 M NaCl): CGU ACU UUU GUA CGU G, UGU ACU UUU GUA CGU G, and UCG AAU UU UUC GAA A.

Pre-*let*-7 Processing

Pre-*let*-7 RNA was incubated with N-terminal histadine-tagged, human Dicer according to the manufacterer's directions (Gene theraphy Systems) or in a standard Drosophilia embryo in vitro RNAi reaction as described previously (Hutvagner etal., 2001; Hutvagner and Zamore, 2002).

Northern Hybridization

Northern hybridization was essentially as described (Hutvágner et al., 2001). 50 mg total RNA was loaded per lane. 5′ 32 P-radiolabeled synthetic RNA probes (Dharmacon) were: 5′-ACA AAU UCG GAU CUA CAG GGU-3′ (to detect miR-10) and 5′-AAA CCU CUC UAG AAC CGA AUU U-3′ (to detect miR-10*). The amount of miR-10 or miR-10* detected was normalized to the non-specific hybridization of the probe to 5S rRNA. Normalizing to hybridization of the probe to a known amount of a miR-10 or miR-10* synthetic RNA control yielded essentially the same result.

ATP-depletion and N-ethyl maleimide (NEM) Inhibition

RNAi reactions using Drosophila embryo lysate were as described (Haley et al., 2003). To compare 'minus' and 'plus' ATP conditions, samples were treated with 10 mM NEM (Pierce) for 10 min at 4°C, then the NEM was quenched with 11 mM dithiothreitol (DTT). For ATP depletion (–ATP), 1 unit of hexokinase and 20 mM (final concentration) glucose were added and the incubation continued for 30 min at 25°C. For 'plus' ATP reactions, 0.05 mg ml–1 (final concentration) creatine kinase and one-tenth volume H2O substituted for hexokinase and glucose. The addition of fresh creatine kinase after NEM treatment did not rescue the defect in RISC assembly, but did restore ATP to high levels (Nykänen et al., 2001). ATP levels were measured using an ATP assay kit (Sigma) and a PhL luminometer (Mediators Diagnostika).

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Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. A method of enhancing the ability of a first strand of a RNAi agent to act as a guide strand in mediating RNAi, comprising lessening the base pair strength between the 5' end of the first strand and the 3' end of a second strand of the duplex as compared to the base pair strength between the 3' end of the first strand and the 5' end of the second strand.

2. A method of enhancing the efficacy of a siRNA duplex, the siRNA duplex comprising a sense and an antisense strand, comprising lessening the base pair strength between the antisense strand 5' end (AS 5') and the sense strand 3' end (S 3') as compared to the base pair strength between the antisense strand 3' end (AS 3') and the sense strand 5' end (S '5), such that efficacy is enhanced.

3. A method of promoting entry of a desired strand of an siRNA duplex into a RISC complex, comprising enhancing the asymmetry of the siRNA duplex, such that entry of the desired strand is promoted.

4. The method of claim 3, wherein asymmetry is enhanced by lessening the base pair strength between the 5' end of the desired strand and the 3' end of a complementary strand of the duplex as compared to the base pair strength between the 3' end of the desired strand and the 5' end of the complementary strand.

5. The method of claim 1 or 2, wherein the base-pair strength is less due to fewer G:C base pairs between the 5' end of the first or antisense strand and the 3' end of the second or sense strand than between the 3' end of the first or antisense strand and the 5' end of the second or sense strand.

6. The method of claim 1 or 2, wherein the base pair strength is less due to at least one mismatched base pair between the 5' end of the first or antisense strand and the 3' end of the second or sense strand.

7. The method of claim 6, wherein the mismatched base pair is selected from the group consisting of G:A, C:A, C:U, G:G, A:A, C:C and U:U.

8. The method of claim 6, wherein the mismatched base pair is selected from the group consisting of G:A, C:A, C:T, G:G, A:A, C:C and U:T.

9. The method of claim 1 or 2, wherein the base pair strength is less due to at least one wobble base pair between the 5' end of the first or antisense strand and the 3' end of the second or sense strand.

10. The method of claim 9, wherein the wobble base pair is G:U.

11. The method of claim 9, wherein the wobble base pair is G:T.

12. The method of claim 1 or 2, wherein the base pair strength is less due to:

(a) at least one mismatched base pair between the 5' end of the first or antisense strand and the 3' end of the second or sense strand; and

(b) at least one wobble base pair between the 5' end of the first or antisense strand and the 3' end of the second or sense strand.

13. The method of claim 12, wherein the mismatched base pair is selected from the group consisting of G:A, C:A, C:U, G:G, A:A, C:C and U:U.

14. The method of claim 12, wherein the mismatched base pair is selected from the group consisting of G:A, C:A, C:T, G:G, A:A, C:C and U:T.

15. The method of claim 12, wherein the wobble base pair is G:U.

16. The method of claim 12, wherein the wobble base pair is G:T.

17. The method of claim 1 or 2, wherein the base pair strength is less due to at least one base pair comprising a rare nucleotide.

18. The method of claim 12, wherein the rare nucleotide is inosine (I).

19. The method of claim 18, wherein the base pair is selected from the group consisting of an I:A, I:U and I:C.

20. The method of claim 1 or 2, wherein the base pair strength is less due to at least one base pair comprising a modified nucleotide.

21. The method of claim 20, wherein the modified nucleotide is selected from the group consisting of 2-amino-G, 2-amino-A, 2,6-diamino-G, and 2,6-diamino-A.

22. The method of claim 1, wherein the RNAi agent is a siRNA duplex.

23. The method of claim 1 or 2, wherein the RNAi agent or siRNA duplex is chemically synthesized.

24. The method of claim 1 or 2, wherein the RNAi agent or siRNA duplex is enzymatically synthesized.

25. The method of claim 1 or 2, wherein the RNAi agent or siRNA duplex is derived from an engineered precursor.

26. A method of enhancing silencing of a target mRNA, comprising contacting a cell having an RNAi pathway with the RNAi agent or siRNA duplex of any one of the preceding claims under conditions such that silencing is enhanced.

27. A method of enhancing silencing of a target mRNA in a subject, comprising administering to the subject a pharmaceutical composition comprising the RNAi agent or siRNA duplex of any one of the preceding claims such that silencing is enhanced.

28. A method of decreasing silencing of an inadvertant target mRNA by a dsRNAi agent, the dsRNAi agent comprising a sense strand and an antisense strand comprising:

(a) detecting a significant degree of complementarity between the sense strand and the inadvertant target; and

(b) enhancing the base pair strength between the 5' end of the sense strand and the 3' end of the antisense strand relative to the base pair strength between the 3' end of the sense strand and the 5' end of the antisense strand;

such that silencing of the inadvertant target mRNA is decreased.

29. The method of claim 28, wherein silencing of the inadvertant target mRNA is decreased relative to silencing of a desired target mRNA.

30. An siRNA duplex comprising a sense strand and an antisense strand, wherein the base pair strength between the antisense strand 5' end (AS 5') and the sense strand 3' end (S 3') is less than the base pair strength between the antisense strand 3' end (AS 3') and the sense strand 5' end (S '5), such that the antisense strand preferentially guides cleavage of a target mRNA.

31. The siRNA duplex of claim 1, wherein the base-pair strength is less due to fewer G:C base pairs between the AS 5' and the S 3' than between the AS 3' and the S 5'.

32. The siRNA duplex of claim 30, wherein the base pair strength is less due to at least one mismatched base pair between the AS 5' and the S 3'.

33. The siRNA duplex of claim 32, wherein the mismatched base pair is selected from the group consisting of G:A, C:A, C:U, G:G, A:A, C:C and U:U.

34. The siRNA duplex of claim 32, wherein the mismatched base pair is selected from the group consisting of G:A, C:A, C:T, G:G, A:A, C:C and U:T.

35. The siRNA duplex of claim 30, wherein the base pair strength is less due to at least one wobble base pair between the AS 5' and the S 3'.

36. The siRNA duplex of claim 32, wherein the wobble base pair is G:U.

37. The siRNA duplex of claim 32, wherein the wobble base pair is G:T.

38. The siRNA duplex of claim 30, wherein the base pair strength is less due to at least one base pair comprising a rare nucleotide.

39. The siRNA duplex of claim 38, wherein the rare nucleotide is inosine (I).

40. The siRNA duplex of claim 39, wherein the base pair is selected from the group consisting of an I:A, I:U and I:C.

41. The siRNA duplex of claim 30, wherein the base pair strength is less due to at least one base pair comprising a modified nucleotide.

42. The siRNA duplex of claim 41, wherein the modified nucleotide is selected from the group consisting of 2-amino-G, 2-amino-A, 2,6-diamino-G, and 2,6-diamino-A.

43. A composition comprising the RNAi agent or siRNA duplex of any one of the preceding claims, formulated to facilitate entry of the RNAi agent or siRNA duplex into a cell.

44. A pharmaceutical composition comprising the RNAi agent or siRNA duplex of any one of the preceding claims.

45. An engineered pre-miRNA comprising the RNAi agent or siRNA duplex of any one of the preceding claims.

46. A vector encoding the pre-miRNA of claim 45.

47. A pri-miRNA comprising the pre-miRNA of claim 46.

48. A vector encoding the pri-miRNA of claim 47.

49. A small hairpin RNA (shRNA) comprising nucleotide sequence identical to the sense and antisense strand of the siRNA duplex of any one of the preceding claims.

50. The shRNA of claim 49, wherein the nucleotide sequence identical to the sense strand is upstream of the nucleotide sequence identical to the antisense strand.

51. The shRNA of claim 49, wherein the nucleotide sequence identical to the antisense strand is upstream of the nucleotide sequence identical to the sense strand.

52. A vector encoding the shRNA of any one of claims 49-51.

53. A cell comprising the vector of any one of claims 46, 48 or 52.

54. The cell of claim 53, which is a mammalian cell.

55. The cell of claim 53, which is a human cell.

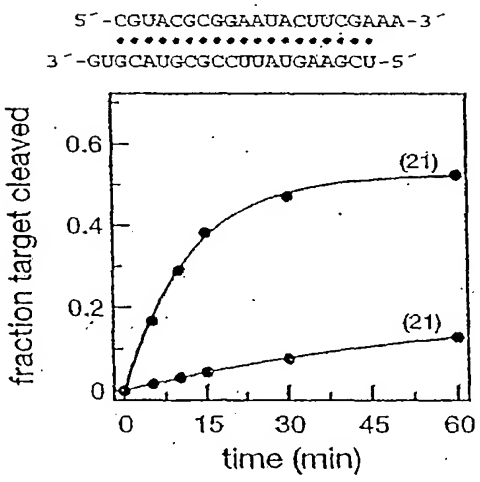
56. A transgene encoding the shRNA of any one of claims 49-51

A

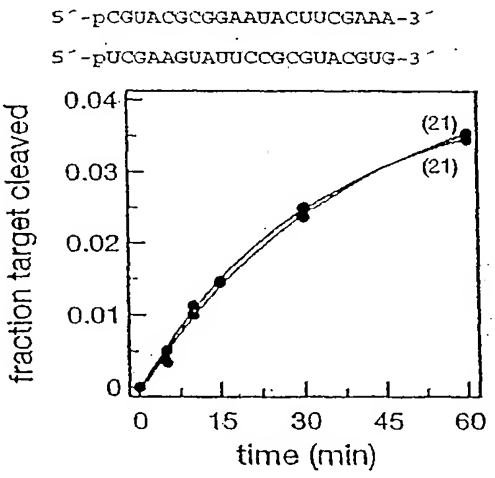
Pp luc sense target: 5´-...cgaggugaacaucacguacgcggaauacuucgaaaugucc...-3´

Pp luc anti-sense target: 3´-...gcuccacuuguagugcaugcgccuuaugaagcuuuacagg...-5´

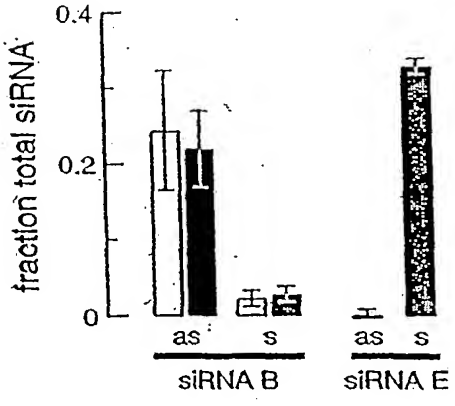
B



C



D



E

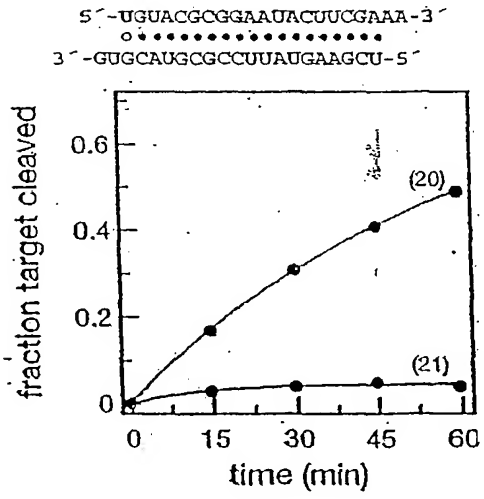


FIGURE 2

A

Pp-luc sense target: 5´-...cgaggugaacaucacguacgcggaauacuucgaaaugucc...-3´

Pp-luc anti-sense target: 3´-...gcuccacuuguagugcaugcgccuuaugaagcuuuacagg...-5´

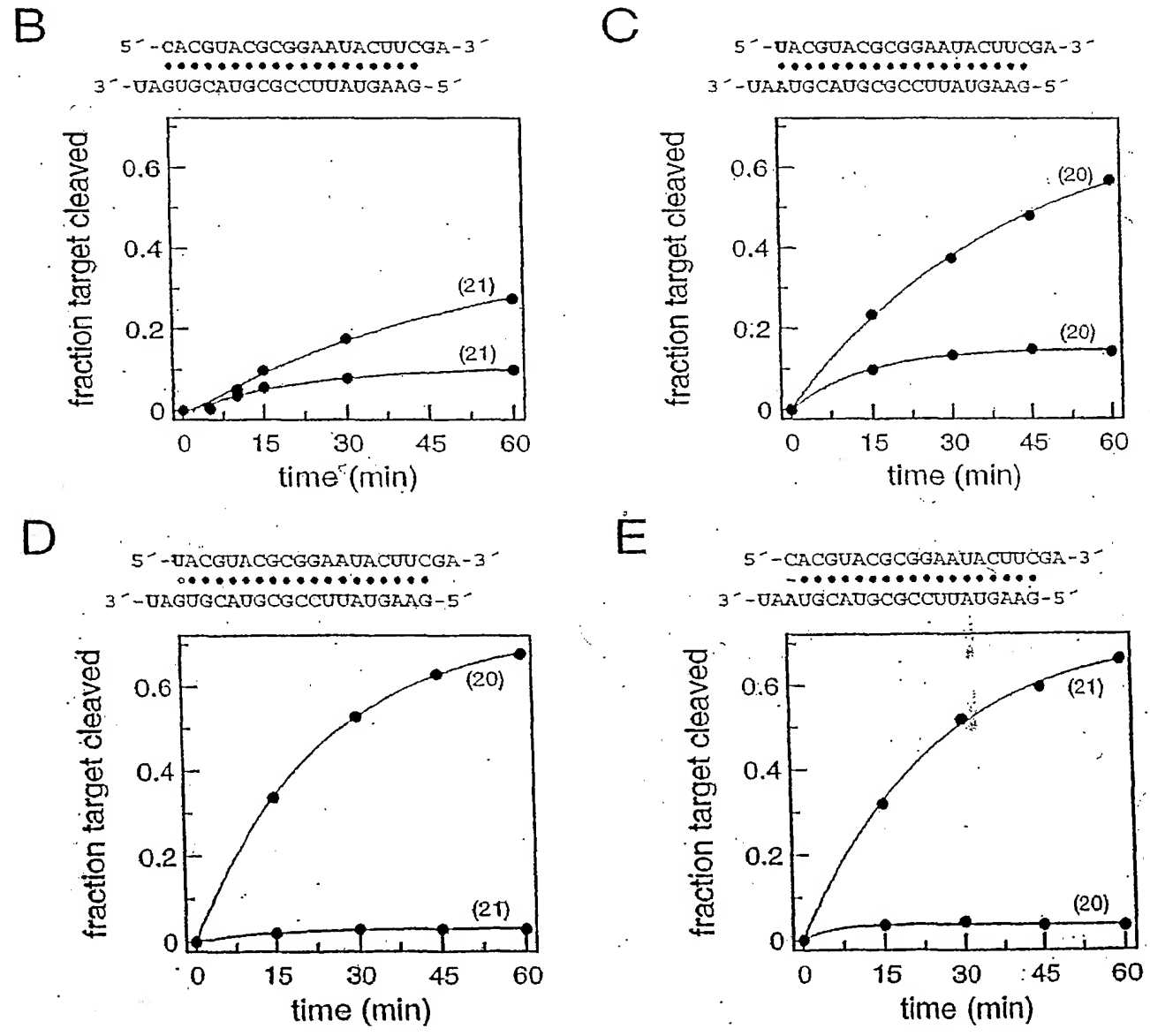


FIGURE 3

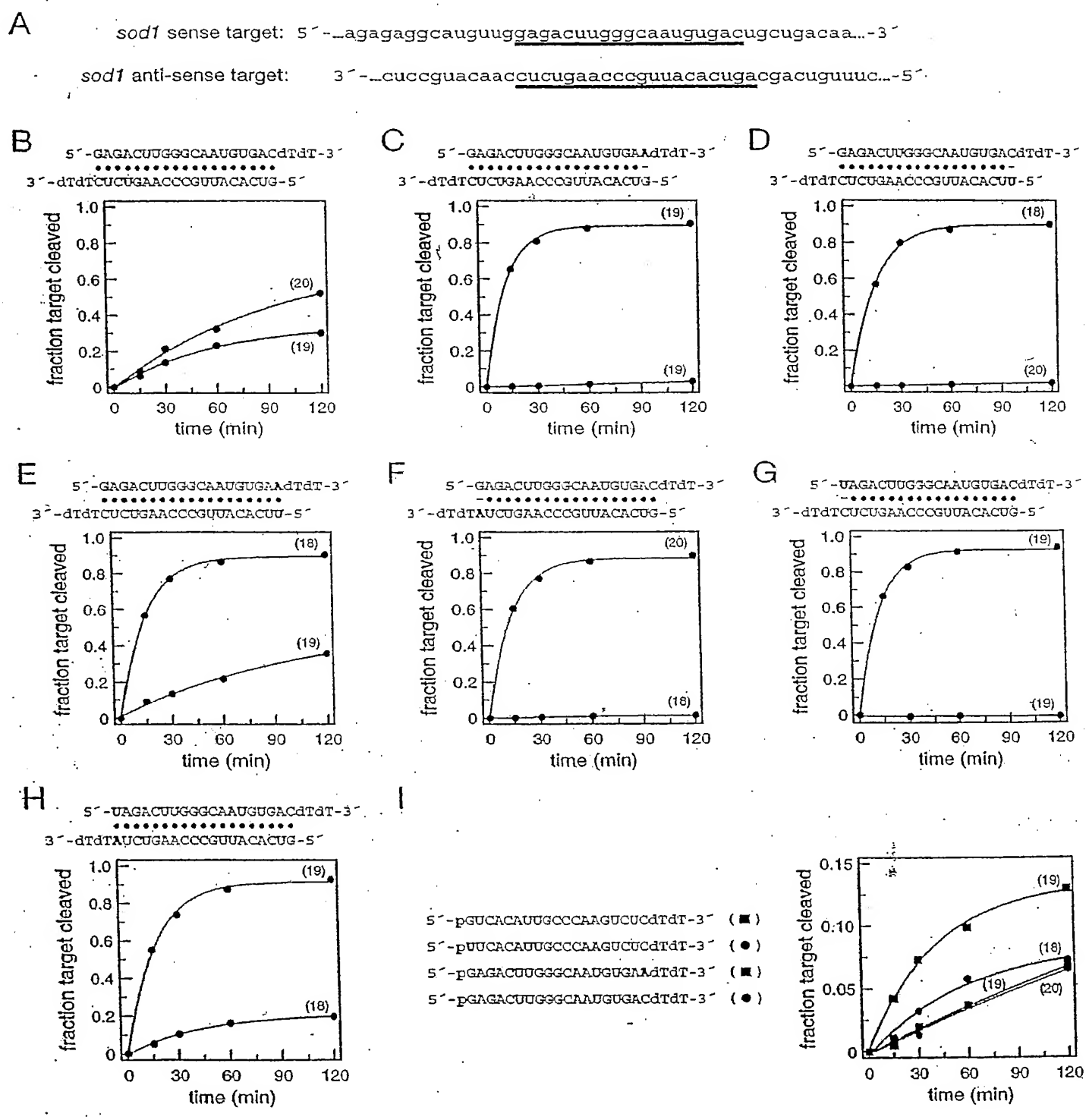

A
sod1 sense target: 5´-...agagaggcauguuggagacuuggggcaaugugacugcugacaa...-3´
sod1 anti-sense target: 3´-...cuccguacaaccucugaacccguuacacugacgacuguuuc...-5´
B
5´-GAGACUUGGGCAAUGUGACdTdT-3´
3´-dTdTCUCUGAACCCGUUACACUG-5´
C
5´-GAGACUUGGGCAAUGUGAAdTdT-3´
3´-dTdTCUCUGAACCCGUUACACUG-5´
D
5´-GAGACUUGGGCAAUGUGACdTdT-3´
3´-dTdTCUCUGAACCCGUUACACUU-5´
E
5´-GAGACUUGGGCAAUGUGAAdTdT-3´
3´-dTdTCUCUGAACCCGUUACACUU-5´
F
5´-GAGACUUGGGCAAUGUGACdTdT-3´
3´-dTdTAUCUGAACCCGUUACACUG-5´
G
5´-UAGACUUGGGCAAUGUGACdTdT-3´
3´-dTdTCUCUGAACCCGUUACACUG-5´
H
5´-UAGACUUGGGCAAUGUGACdTdT-3´
3´-dTdTAUCUGAACCCGUUACACUG-5´
I
5´-pGUCACAUUGCCCAAGUCUCdTdT-3´ (■)
5´-pUUCACAUUGCCCAAGUCUCdTdT-3´ (●)
5´-pGAGACUUGGGCAAUGUGAAdTdT-3´ (■)
5´-pGAGACUUGGGCAAUGUGACdTdT-3´ (●)
fraction target cleaved
time (min)

FIGURE 4

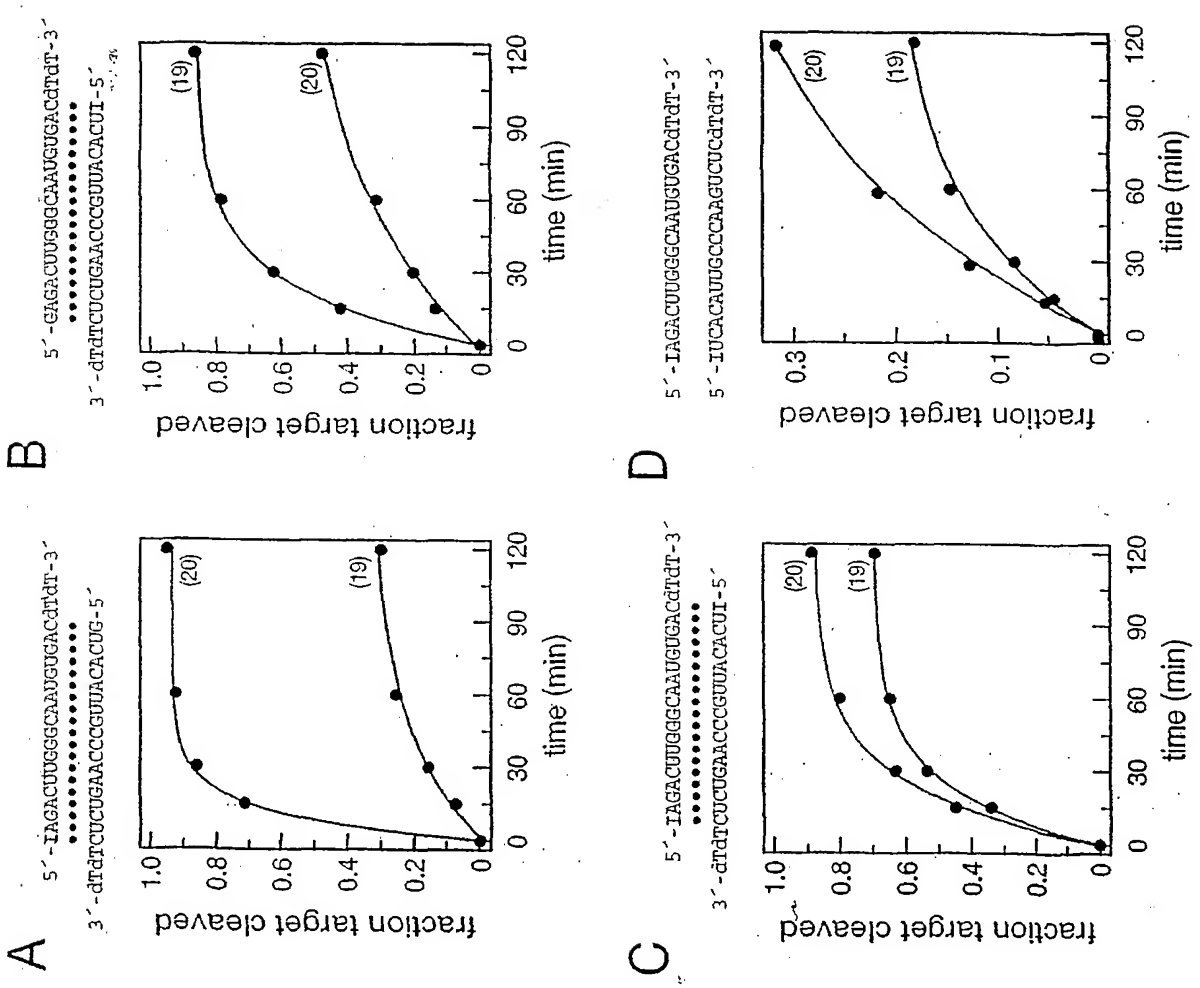

A
B
C
D
fraction target cleaved
time (min)
(19)
(20)
0
0.2
0.4
0.6
0.8
1.0
0.1
0.3
0
30
60
90
120

FIGURE 5

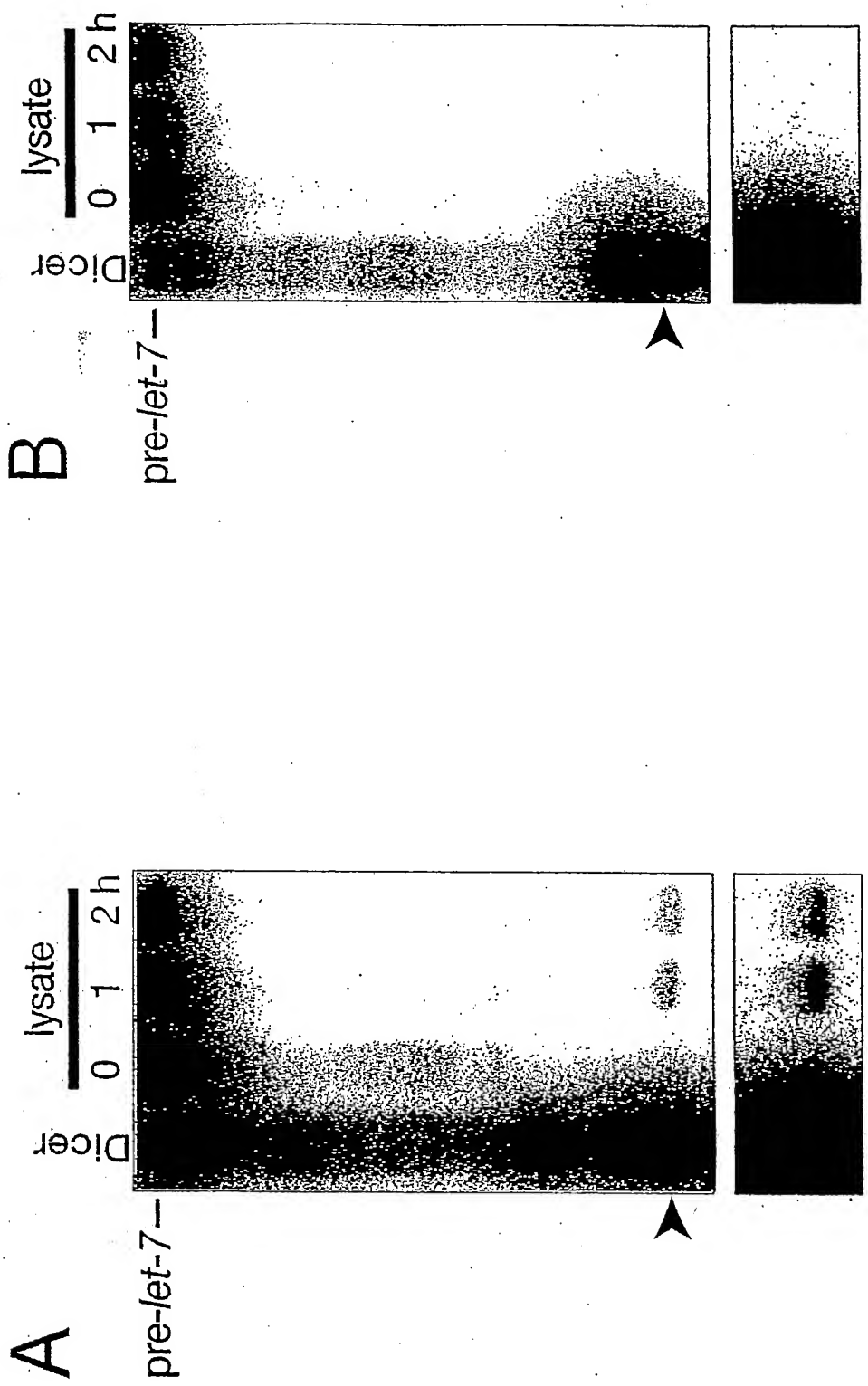


FIGURE 6

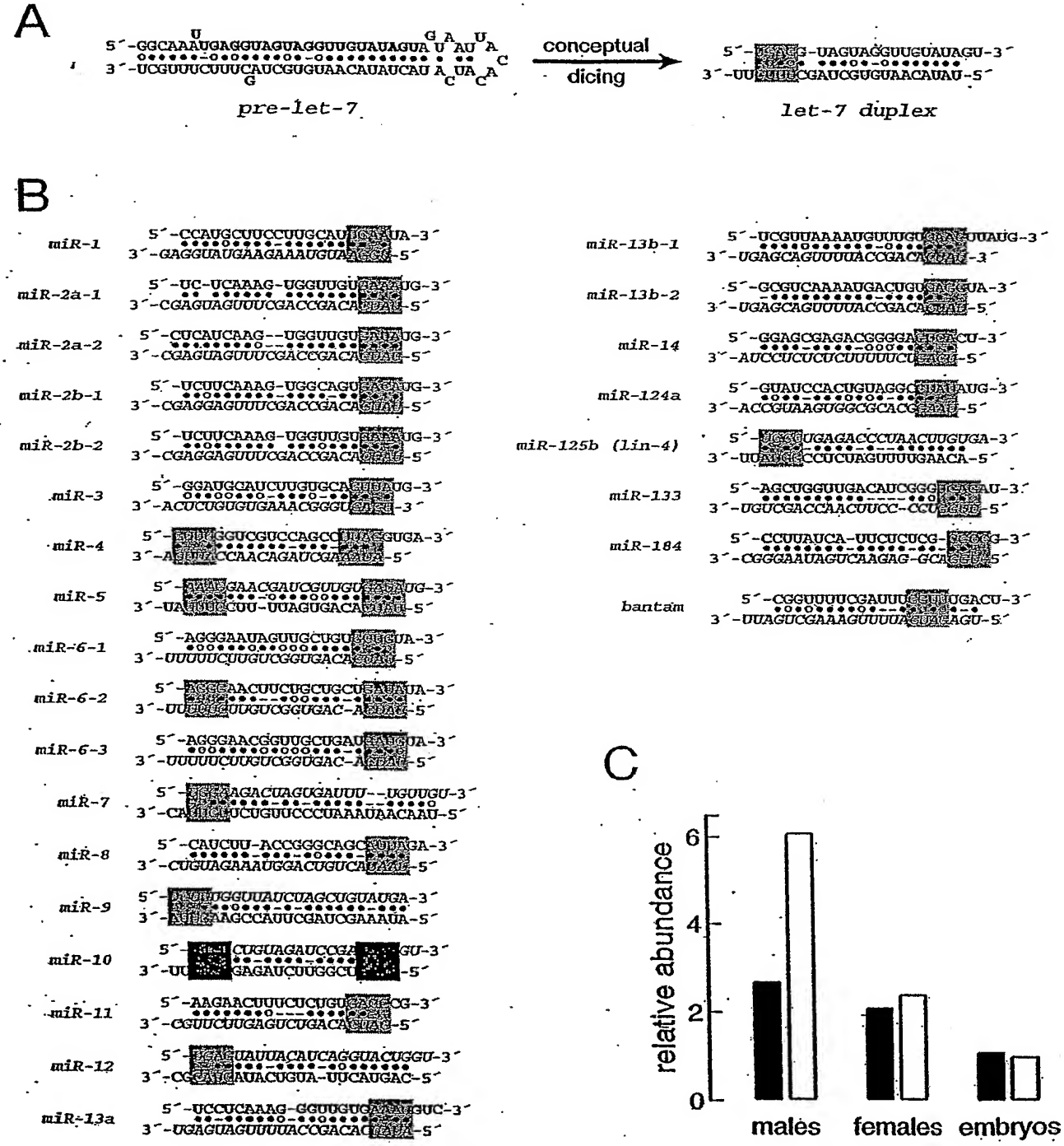

A
5′-GGCAAAUGAGGUAGUAGGUUGUAUAGUA
3′-UCGUUUCUUUCAUCGUGUAACAUAUCAU
pre-let-7
conceptual
dicing
5′-UAGUAGGUUGUAUAGU-3′
3′-UUCGAUCGUGUAACAUAU-5′
let-7 duplex
B
miR-1
miR-2a-1
miR-2a-2
miR-2b-1
miR-2b-2
miR-3
miR-4
miR-5
miR-6-1
miR-6-2
miR-6-3
miR-7
miR-8
miR-9
miR-10
miR-11
miR-12
miR-13a
miR-13b-1
miR-13b-2
miR-14
miR-124a
miR-125b (lin-4)
miR-133
miR-184
bantam
C
relative abundance
0
2
4
6
males
females
embryos

FIGURE 7

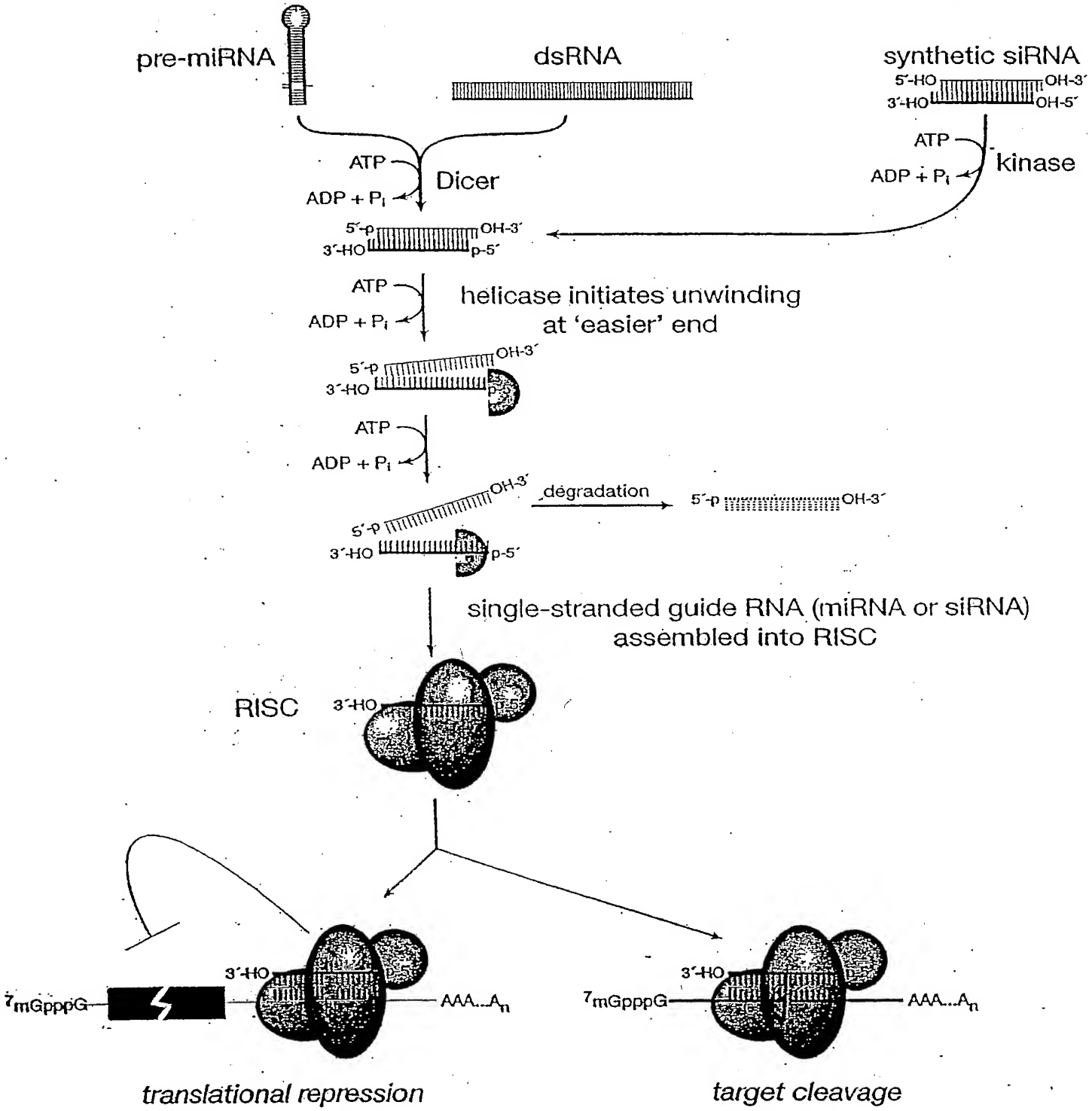

pre-miRNA
dsRNA
synthetic siRNA
5′-HO
OH-3′
3′-HO
OH-5′
ATP
ADP + Pi
Dicer
kinase
5′-p
OH-3′
3′-HO
p-5′
helicase initiates unwinding
at 'easier' end
dégradation
single-stranded guide RNA (miRNA or siRNA)
assembled into RISC
RISC
7mGpppG
AAA...An
translational repression
target cleavage

FIGURE 8

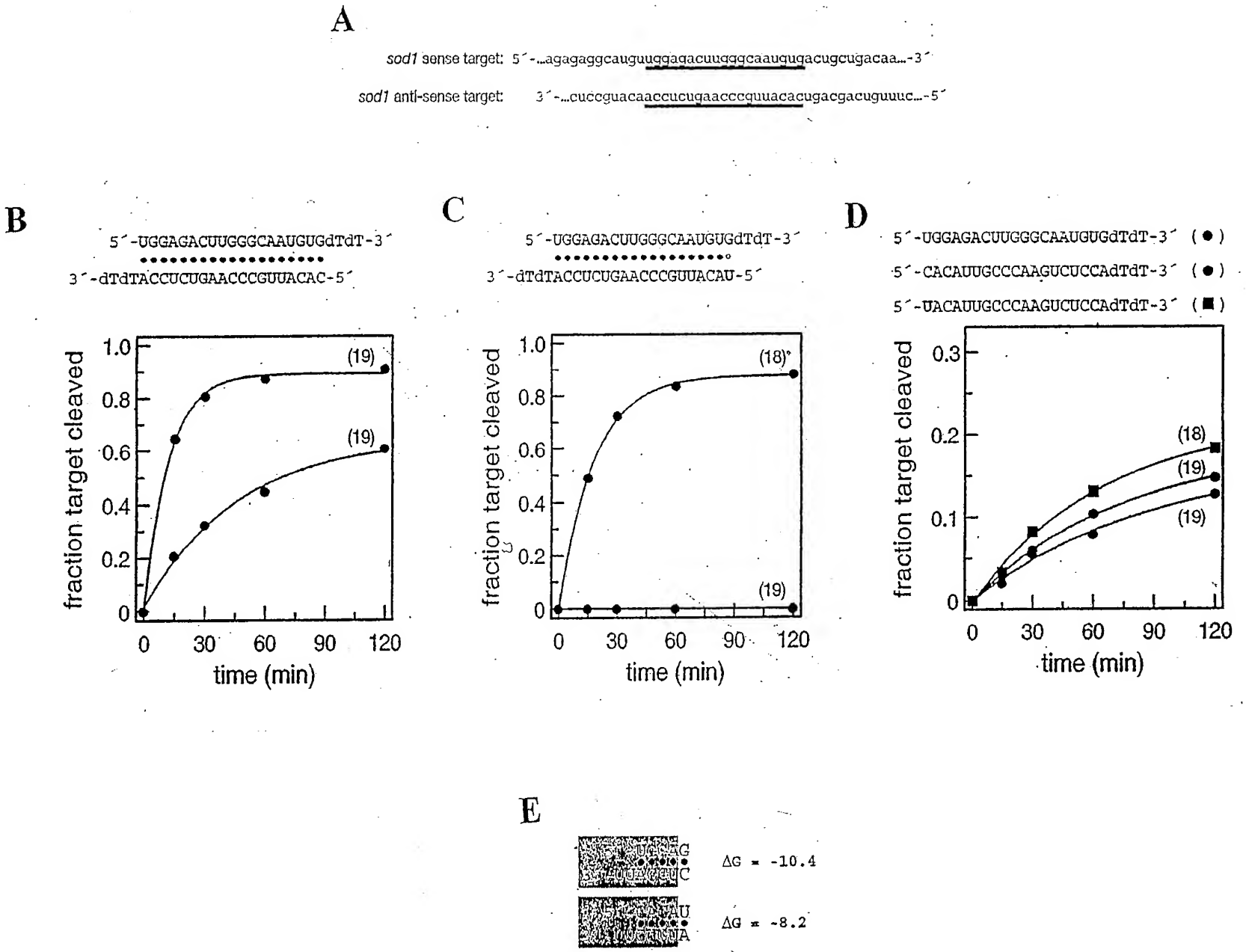

A
sod1 sense target: 5´-...agagaggcauguuggagacuuggcaauguqacugcugacaa...-3´
sod1 anti-sense target: 3´-...cuccguacaaccucugaacccguuacacugacgacuguuuc...-5´
B
5´-UGGAGACUUGGGCAAUGUGdTdT-3´
3´-dTdTACCUCUGAACCCGUUACAC-5´
fraction target cleaved
time (min)
(19)
(19)
C
5´-UGGAGACUUGGGCAAUGUGdTdT-3´
3´-dTdTACCUCUGAACCCGUUACAU-5´
fraction target cleaved
time (min)
(18)*
(19)
D
5´-UGGAGACUUGGGCAAUGUGdTdT-3´ (●)
5´-CACAUUGCCCAAGUCUCCAdTdT-3´ (●)
5´-UACAUUGCCCAAGUCUCCAdTdT-3´ (■)
fraction target cleaved
time (min)
(18)
(19)
(19)
E
ΔG = -10.4
ΔG = -8.2

FIGURE 9

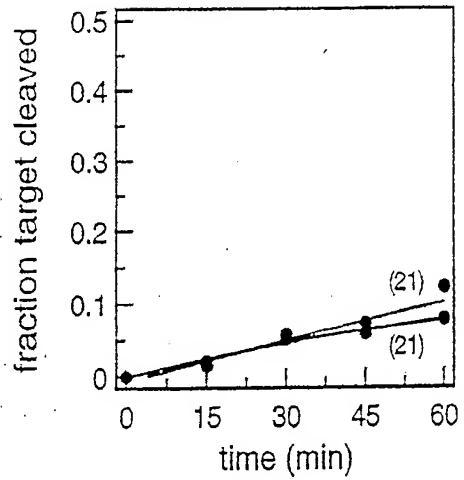
A

htt sense target: 5´-...ugcagcugaucaucgaugugcugacccugaggaacaguuc...-3´

htt anti-sense target: 3´-...acgucgacuaguagcuacacgacugggacuccuugucaag...-5´

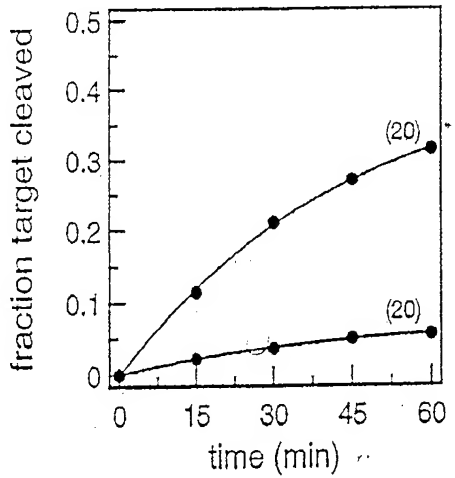
B

5´-UGUGCUGACCCUGAGGAACAG-3´
3´-CUACACGACUGGGACUCCUUG-5´



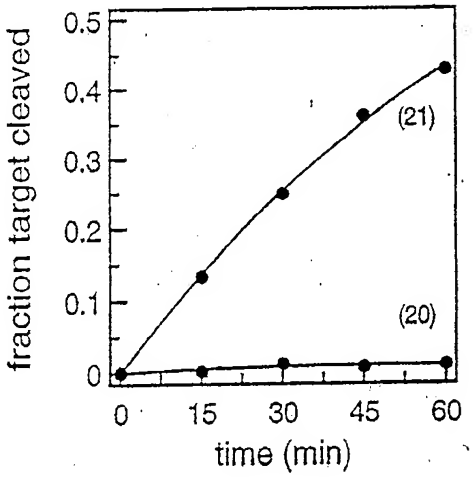
C

5´-UGUGCUGACCCUGAGGAAAAG-3´
3´-CUACACGACUGGGACUCCUUU-5´



D

5´-UGUGCUGACCCUGAGGAAAAG-3´
3´-CUACACGACUGGGACUCCUUG-5´



E

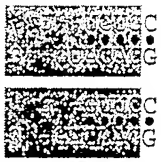
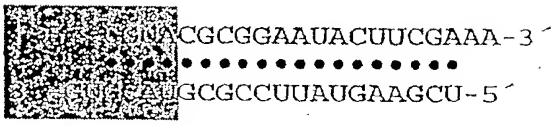
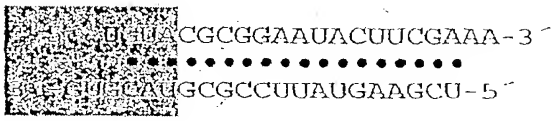


FIGURE 10



5´-CGUA
3´-GUGCAU

ΔG = -8.7 kcal/mol

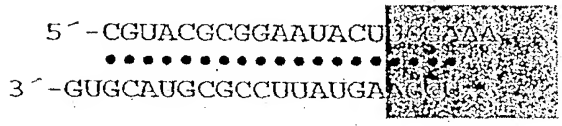


5´-U
GUA
CAU
3´-GUG

ΔG = -7.4 kcal/mol

5´-UGUA
3´-GUGCAU

ΔG = -7.2 kcal/mol



5´-UCGA
3´-AAAGCU

ΔG = -8.4 kcal/mol

FIGURE 11

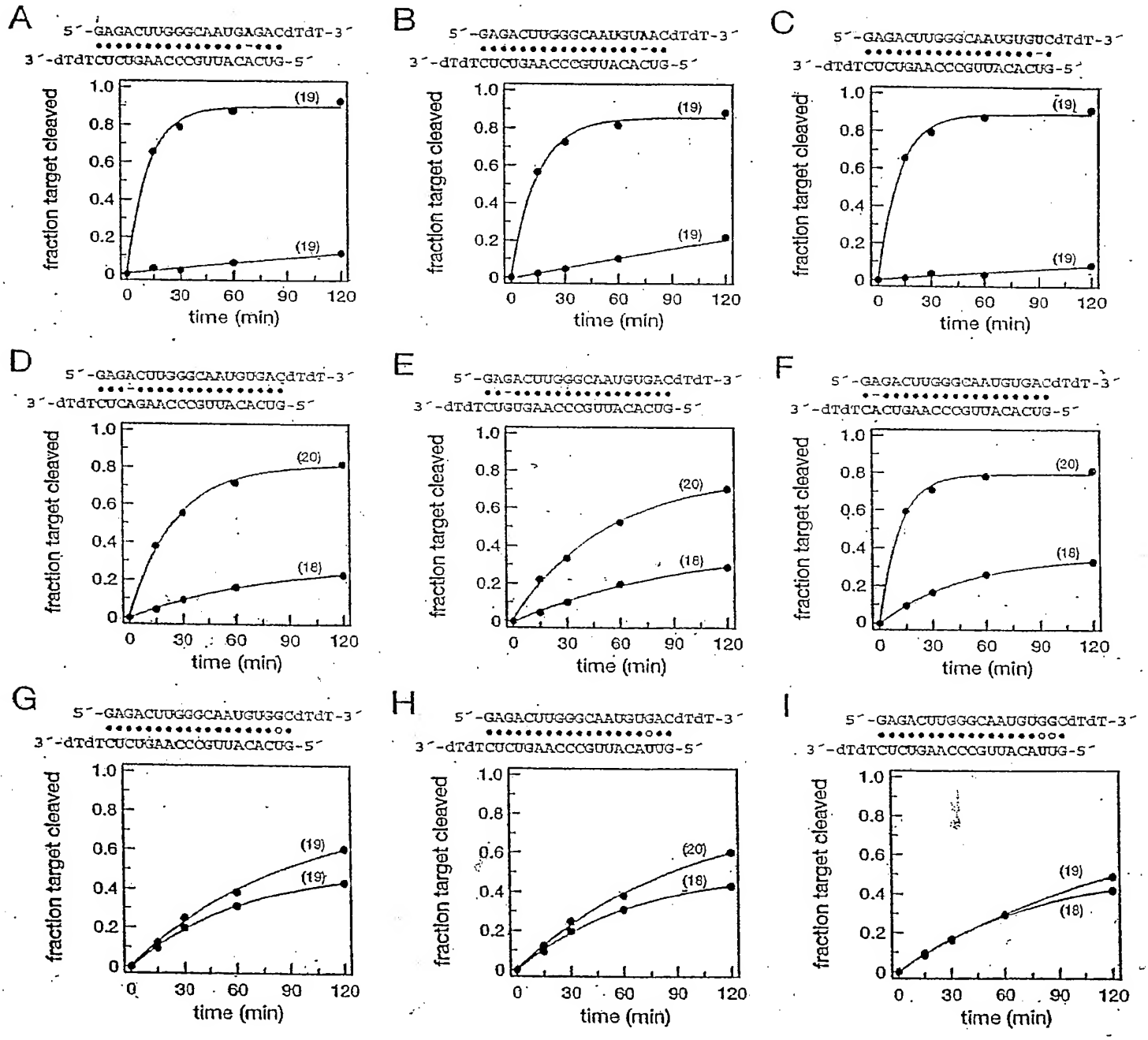

A
5′-GAGACUUGGGCAAUGAGACdTdT-3′
3′-dTdTCUCUGAACCCGUUACACUG-5′
B
5′-GAGACUUGGGCAAUGUAACdTdT-3′
3′-dTdTCUCUGAACCCGUUACACUG-5′
C
5′-GAGACUUGGGCAAUGUGUCdTdT-3′
3′-dTdTCUCUGAACCCGUUACACUG-5′
D
5′-GAGACUUGGGCAAUGUGACdTdT-3′
3′-dTdTCUCAGAACCCGUUACACUG-5′
E
5′-GAGACUUGGGCAAUGUGACdTdT-3′
3′-dTdTCUGUGAACCCGUUACACUG-5′
F
5′-GAGACUUGGGCAAUGUGACdTdT-3′
3′-dTdTCACUGAACCCGUUACACUG-5′
G
5′-GAGACUUGGGCAAUGUGGCdTdT-3′
3′-dTdTCUCUGAACCCGUUACACUG-5′
H
5′-GAGACUUGGGCAAUGUGACdTdT-3′
3′-dTdTCUCUGAACCCGUUACAUUG-5′
I
5′-GAGACUUGGGCAAUGUGGCdTdT-3′
3′-dTdTCUCUGAACCCGUUACAUUG-5′
fraction target cleaved
time (min)
0
30
60
90
120
0.2
0.4
0.6
0.8
1.0
(19)
(20)
(18)

FIGURE 12

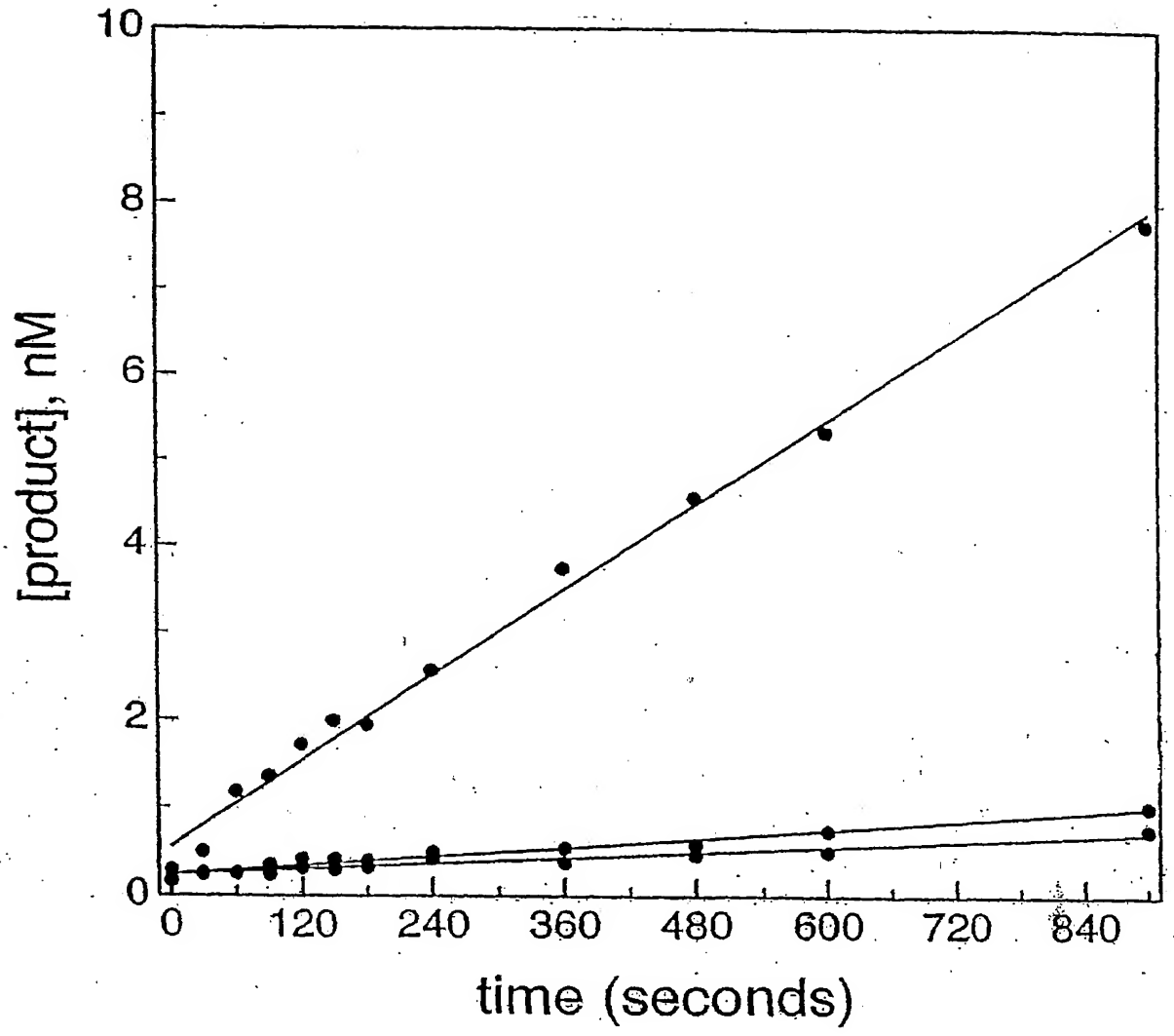


FIGURE 13

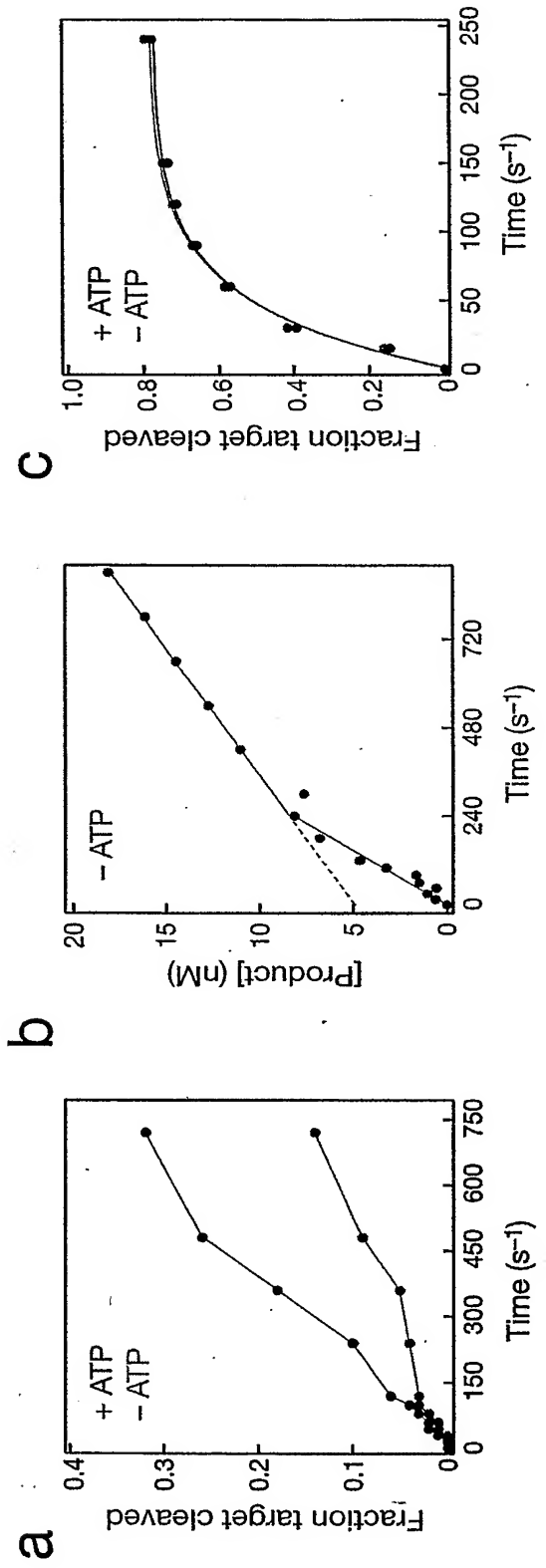

a
Fraction target cleaved
+ ATP
– ATP
Time (s⁻¹)
b
[Product] (nM)
– ATP
Time (s⁻¹)
c
Fraction target cleaved
+ ATP
– ATP
Time (s⁻¹)

FIGURE 14

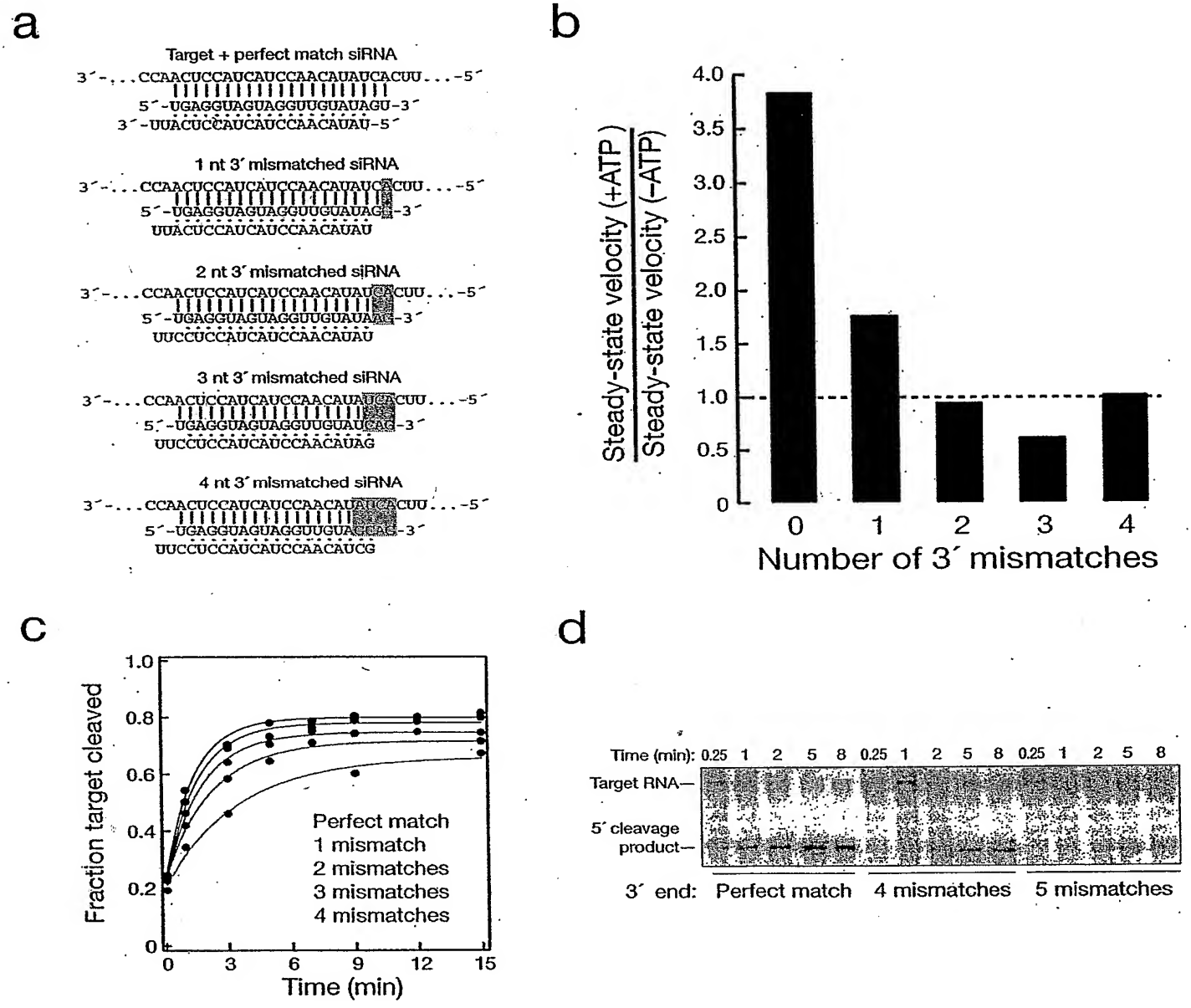

a
Target + perfect match siRNA
3′-...CCAACUCCAUCAUCCAACAUAUCACUU...-5′
5′-UGAGGUAGUAGGUUGUAUAGU-3′
3′-UUACUCCAUCAUCCAACAUAU-5′
1 nt 3′ mismatched siRNA
3′-...CCAACUCCAUCAUCCAACAUAUCACUU...-5′
5′-UGAGGUAGUAGGUUGUAUAGC-3′
UUACUCCAUCAUCCAACAUAU
2 nt 3′ mismatched siRNA
3′-...CCAACUCCAUCAUCCAACAUAUCACUU...-5′
5′-UGAGGUAGUAGGUUGUAUAAC-3′
UUCCUCCAUCAUCCAACAUAU
3 nt 3′ mismatched siRNA
3′-...CCAACUCCAUCAUCCAACAUAUCACUU...-5′
5′-UGAGGUAGUAGGUUGUAUCAC-3′
UUCCUCCAUCAUCCAACAUAG
4 nt 3′ mismatched siRNA
3′-...CCAACUCCAUCAUCCAACAUAUCACUU...-5′
5′-UGAGGUAGUAGGUUGUAGCAC-3′
UUCCUCCAUCAUCCAACAUCG
b
Steady-state velocity (+ATP) / Steady-state velocity (−ATP)
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0
0 1 2 3 4
Number of 3′ mismatches
c
Fraction target cleaved
1.0
0.8
0.6
0.4
0.2
0
0 3 6 9 12 15
Time (min)
Perfect match
1 mismatch
2 mismatches
3 mismatches
4 mismatches
d
Time (min): 0.25 1 2 5 8 0.25 1 2 5 8 0.25 1 2 5 8
Target RNA—
5′ cleavage product—
3′ end: Perfect match 4 mismatches 5 mismatches

FIGURE 15

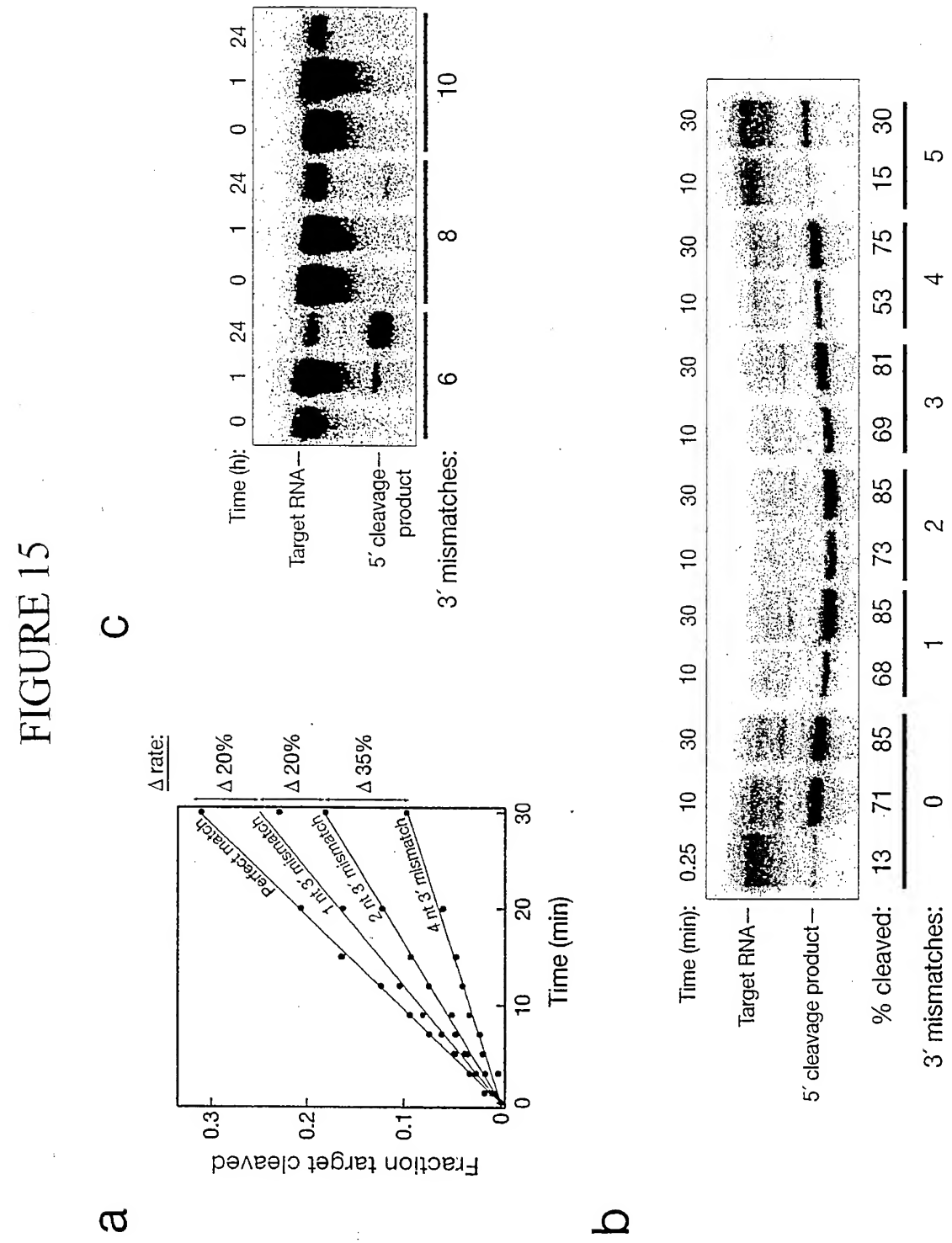

a
Fraction target cleaved
Time (min)
Δ rate:
Δ 20%
Δ 20%
Δ 35%
Perfect match
1 nt 3´ mismatch
2 nt 3´ mismatch
4 nt 3´ mismatch
b
Time (min):
Target RNA
5´ cleavage product
% cleaved:
3´ mismatches:
c
Time (h):
Target RNA
5´ cleavage product
3´ mismatches:

FIGURE 16

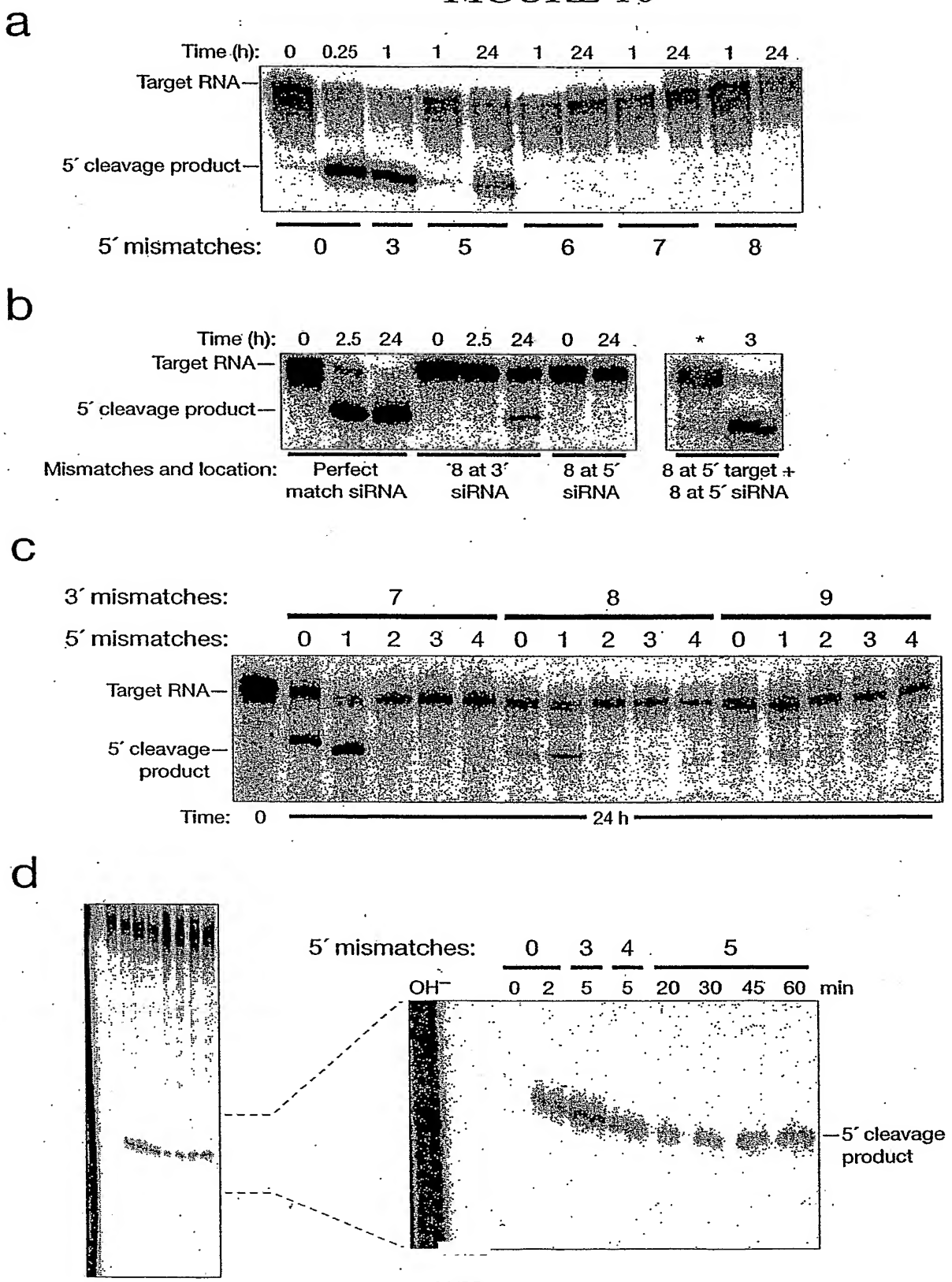

a
Time (h): 0 0.25 1 1 24 1 24 1 24 1 24
Target RNA
5′ cleavage product
5′ mismatches: 0 3 5 6 7 8
b
Time (h): 0 2.5 24 0 2.5 24 0 24 * 3
Target RNA
5′ cleavage product
Mismatches and location: Perfect match siRNA
8 at 3′ siRNA
8 at 5′ siRNA
8 at 5′ target + 8 at 5′ siRNA
c
3′ mismatches: 7 8 9
5′ mismatches: 0 1 2 3 4 0 1 2 3 4 0 1 2 3 4
Target RNA
5′ cleavage product
Time: 0 24 h
d
5′ mismatches: 0 3 4 5
OH⁻ 0 2 5 5 20 30 45 60 min
5′ cleavage product

FIGURE 17

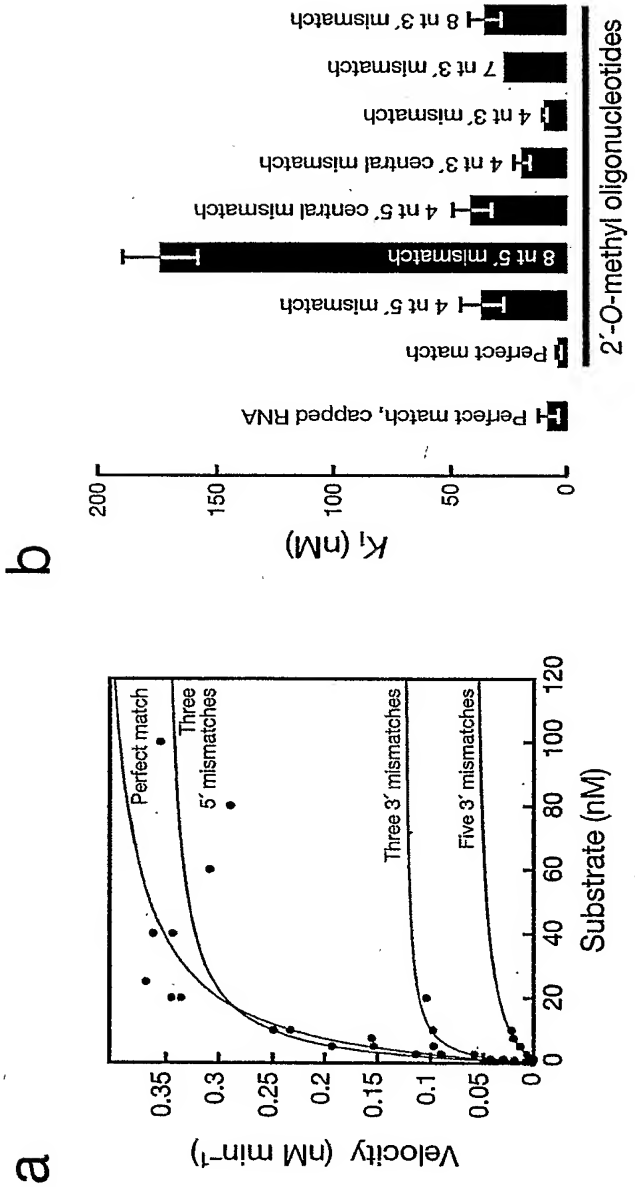

a
Velocity (nM min⁻¹)
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
0 20 40 60 80 100 120
Substrate (nM)
Perfect match
Three 5′ mismatches
Three 3′ mismatches
Five 3′ mismatches
b
K_i (nM)
200
150
100
50
0
Perfect match, capped RNA
Perfect match
4 nt 5′ mismatch
8 nt 5′ mismatch
4 nt 5′ central mismatch
4 nt 3′ central mismatch
4 nt 3′ mismatch
7 nt 3′ mismatch
8 nt 3′ mismatch
2′-O-methyl oligonucleotides

FIGURE 18

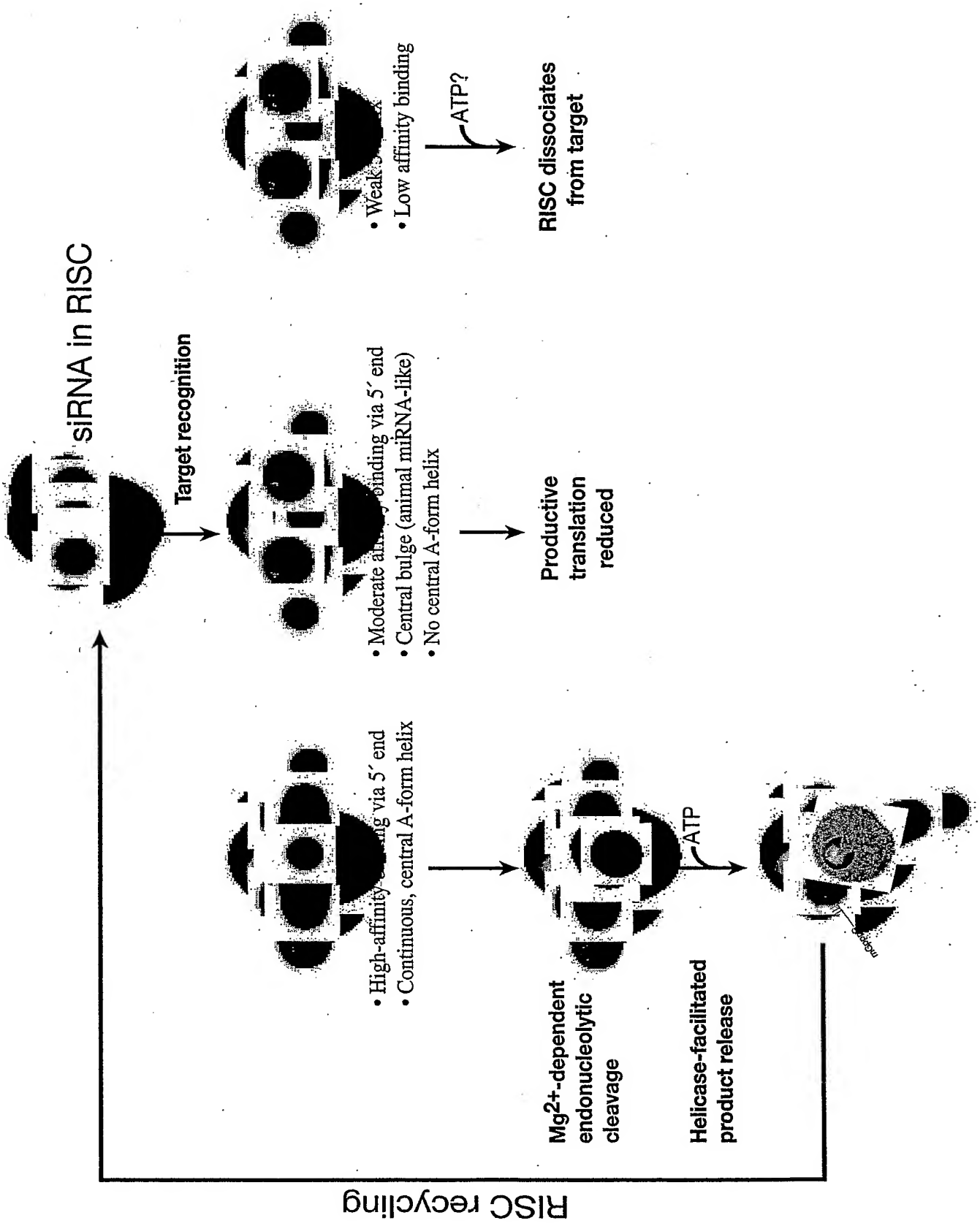

siRNA in RISC
Target recognition
• Moderate affinity binding via 5′ end
• Central bulge (animal miRNA-like)
• No central A-form helix
• Weak
• Low affinity binding
ATP?
RISC dissociates from target
Productive translation reduced
• High-affinity binding via 5′ end
• Continuous, central A-form helix
Mg2+-dependent endonucleolytic cleavage
ATP
Helicase-facilitated product release
RISC recycling

FIGURE 19

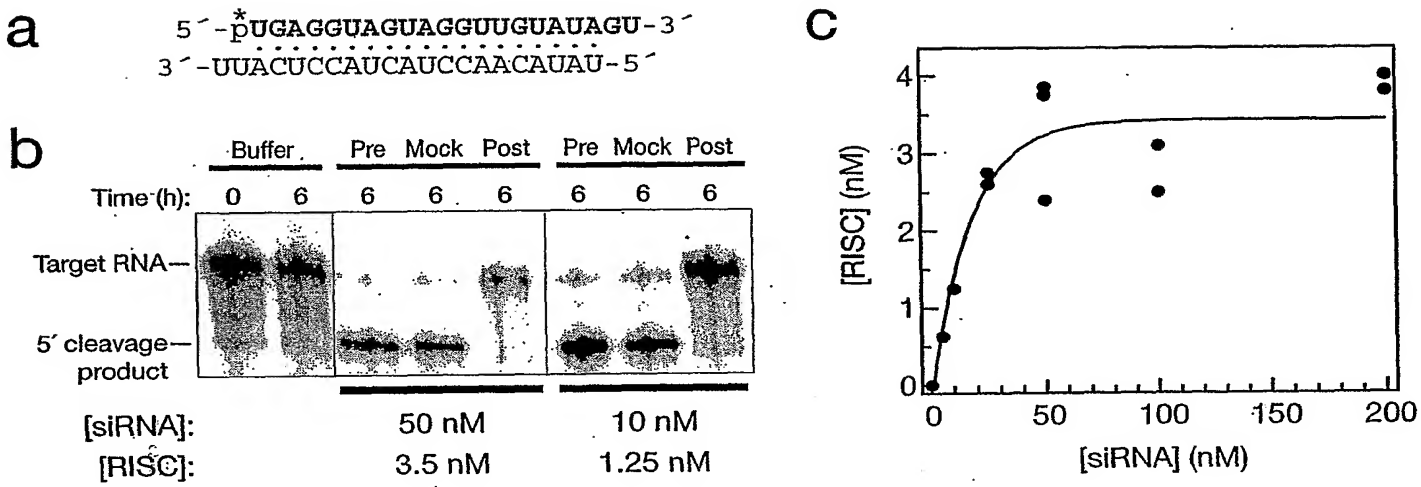
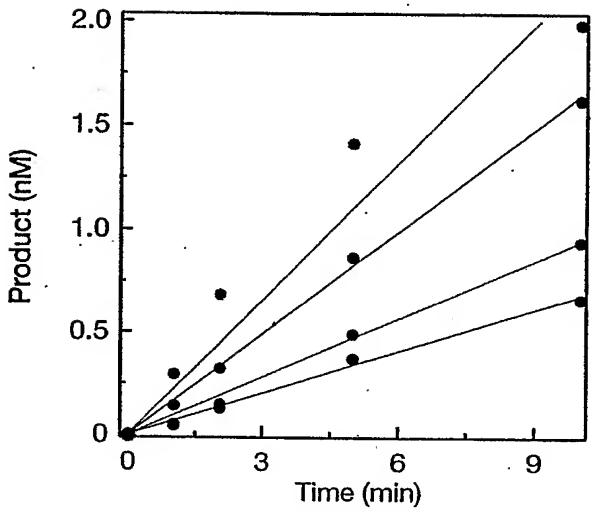

a
5´-*pUGAGGUAGUAGGUUGUAUAGU-3´
3´-UUACUCCAUCAUCCAACAUAU-5´
b
Buffer
Pre Mock Post
Pre Mock Post
Time (h):
0 6 6 6 6 6 6 6
Target RNA—
5´ cleavage—
product
[siRNA]:
50 nM
10 nM
[RISC]:
3.5 nM
1.25 nM
c
[RISC] (nM)
0 1 2 3 4
0 50 100 150 200
[siRNA] (nM)

FIGURE 20

a


2.0
1.5
1.0
0.5
0
Product (nM)
0
3
6
9
Time (min)

b

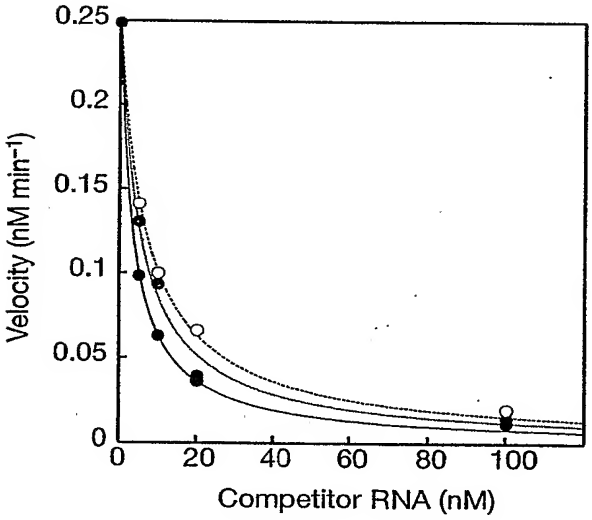
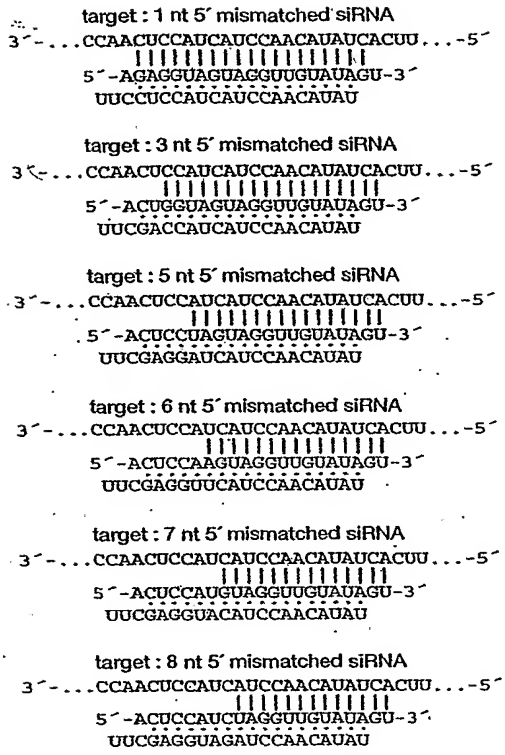

0.25
0.2
0.15
0.1
0.05
0
Velocity (nM min-1)
0
20
40
60
80
100
Competitor RNA (nM)

FIGURE 21

Target and siRNA	Figure #
target : fully matched siRNA 3´-...CCAACUCCAUCAUCCAACAUAUCACUU...-5´ 5´-UGAGGUAGUAGGUUGUAUAGU-3´ 3´-UUACUCCAUCAUCCAACAUAU-5´ target : 1 nt 3´ mismatched siRNA 3´-...CCAACUCCAUCAUCCAACAUAUCACUU...-5´ 5´-UGAGGUAGUAGGUUGUAUAGG-3´ UUACUCCAUCAUCCAACAUAU target : 2 nt 3´ mismatched siRNA 3´-...CCAACUCCAUCAUCCAACAUAUCACUU...-5´ 5´-UGAGGUAGUAGGUUGUAUAAG-3´ UUCCUCCAUCAUCCAACAUAU target : 3 nt 3´ mismatched siRNA 3´-...CCAACUCCAUCAUCCAACAUAUCACUU...-5´ 5´-UGAGGUAGUAGGUUGUAUCAG-3´ UUCCUCCAUCAUCCAACAUAG target : 4 nt 3´ mismatched siRNA 3´-...CCAACUCCAUCAUCCAACAUAUCACUU...-5´ 5´-UGAGGUAGUAGGUUGUAGCAG-3´ UUCCUCCAUCAUCCAACAUCG target : 5 nt 3´ mismatched siRNA 3´-...CCAACUCCAUCAUCCAACAUAUCACUU...-5´ 5´-UGAGGUAGUAGGUUGUUGCAG-3´ UUCCUCCAUCAUCCAACAACG	Figures 2b-d, 3a,b and 5a
target : 6 nt 3´ mismatched siRNA 3´-...CCAACUCCAUCAUCCAACAUAUCACUU...-5´ 5´-UGAGGUAGUAGGUUGAUGCAG-3´ UUCCUCCAUCAUCCAACUACG target : 8 nt 3´ mismatched siRNA 3´-...CCAACUCCAUCAUCCAACAUAUCACUU...-5´ 5´-UGAGGUAGUAGGUACAUGCAG-3´ UUCCUCCAUCAUCCAAGUACG target : 10 nt 3´ mismatched siRNA 3´-...CCAACUCCAUCAUCCAACAUAUCACUU...-5´ 5´-UGAGGUAGUAGCAACAUGCAG-3´ UUCCUCCAUCAUCCUUGUACG	Figure 3c



Figures 4a, d and 5a

Figure 4b

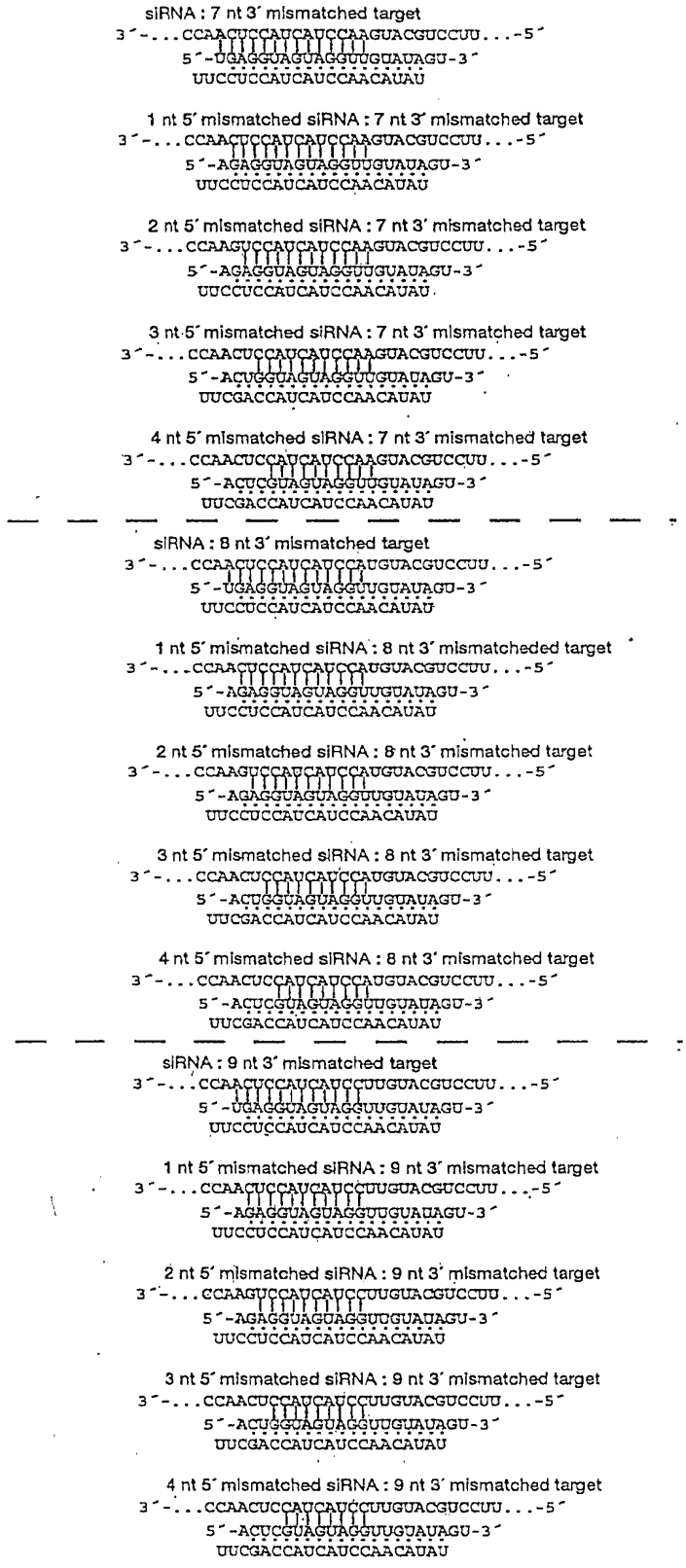

siRNA : 7 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCAAGUACGUCCUU...-5′
5′-UGAGGUAGUAGGUUGUAUAGU-3′
UUCCUCCAUCAUCCAACAUAU
1 nt 5′ mismatched siRNA : 7 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCAAGUACGUCCUU...-5′
5′-AGAGGUAGUAGGUUGUAUAGU-3′
UUCCUCCAUCAUCCAACAUAU
2 nt 5′ mismatched siRNA : 7 nt 3′ mismatched target
3′-...CCAAGUCCAUCAUCCAAGUACGUCCUU...-5′
5′-AGAGGUAGUAGGUUGUAUAGU-3′
UUCCUCCAUCAUCCAACAUAU
3 nt 5′ mismatched siRNA : 7 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCAAGUACGUCCUU...-5′
5′-ACUGGUAGUAGGUUGUAUAGU-3′
UUCGACCAUCAUCCAACAUAU
4 nt 5′ mismatched siRNA : 7 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCAAGUACGUCCUU...-5′
5′-ACUCGUAGUAGGUUGUAUAGU-3′
UUCGACCAUCAUCCAACAUAU
siRNA : 8 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCAUGUACGUCCUU...-5′
5′-UGAGGUAGUAGGUUGUAUAGU-3′
UUCCUCCAUCAUCCAACAUAU
1 nt 5′ mismatched siRNA : 8 nt 3′ mismatcheded target
3′-...CCAACUCCAUCAUCCAUGUACGUCCUU...-5′
5′-AGAGGUAGUAGGUUGUAUAGU-3′
UUCCUCCAUCAUCCAACAUAU
2 nt 5′ mismatched siRNA : 8 nt 3′ mismatched target
3′-...CCAAGUCCAUCAUCCAUGUACGUCCUU...-5′
5′-AGAGGUAGUAGGUUGUAUAGU-3′
UUCCUCCAUCAUCCAACAUAU
3 nt 5′ mismatched siRNA : 8 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCAUGUACGUCCUU...-5′
5′-ACUGGUAGUAGGUUGUAUAGU-3′
UUCGACCAUCAUCCAACAUAU
4 nt 5′ mismatched siRNA : 8 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCAUGUACGUCCUU...-5′
5′-ACUCGUAGUAGGUUGUAUAGU-3′
UUCGACCAUCAUCCAACAUAU
siRNA : 9 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCUUGUACGUCCUU...-5′
5′-UGAGGUAGUAGGUUGUAUAGU-3′
UUCCUCCAUCAUCCAACAUAU
1 nt 5′ mismatched siRNA : 9 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCUUGUACGUCCUU...-5′
5′-AGAGGUAGUAGGUUGUAUAGU-3′
UUCCUCCAUCAUCCAACAUAU
2 nt 5′ mismatched siRNA : 9 nt 3′ mismatched target
3′-...CCAAGUCCAUCAUCCUUGUACGUCCUU...-5′
5′-AGAGGUAGUAGGUUGUAUAGU-3′
UUCCUCCAUCAUCCAACAUAU
3 nt 5′ mismatched siRNA : 9 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCUUGUACGUCCUU...-5′
5′-ACUGGUAGUAGGUUGUAUAGU-3′
UUCGACCAUCAUCCAACAUAU
4 nt 5′ mismatched siRNA : 9 nt 3′ mismatched target
3′-...CCAACUCCAUCAUCCUUGUACGUCCUU...-5′
5′-ACUCGUAGUAGGUUGUAUAGU-3′
UUCGACCAUCAUCCAACAUAU

Figure 4c

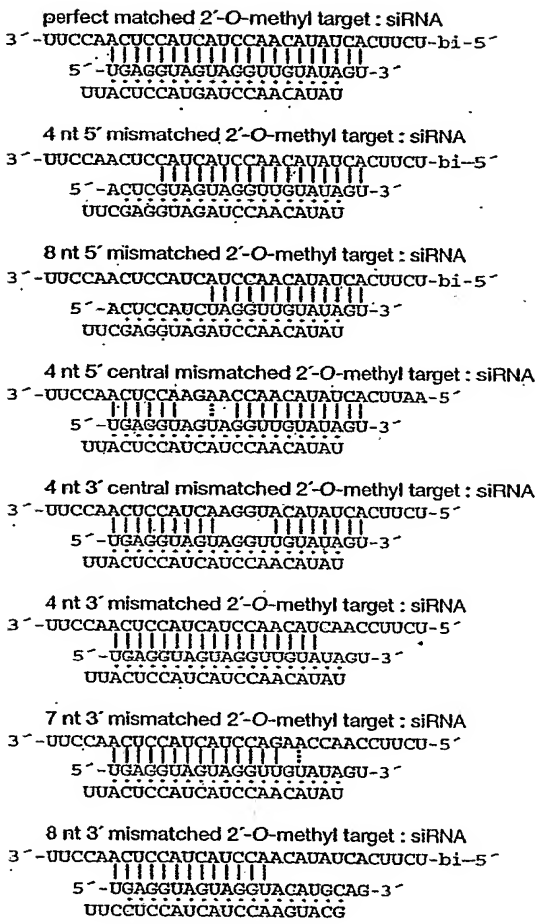

perfect matched 2′-O-methyl target : siRNA
3′-UUCCAACUCCAUCAUCCAACAUAUCACUUCU-bi-5′
5′-UGAGGUAGUAGGUUGUAUAGU-3′
UUACUCCAUGAUCCAACAUAU
4 nt 5′ mismatched 2′-O-methyl target : siRNA
3′-UUCCAACUCCAUCAUCCAACAUAUCACUUCU-bi-5′
5′-ACUCGUAGUAGGUUGUAUAGU-3′
UUCGAGGUAGAUCCAACAUAU
8 nt 5′ mismatched 2′-O-methyl target : siRNA
3′-UUCCAACUCCAUCAUCCAACAUAUCACUUCU-bi-5′
5′-ACUCCAUCUAGGUUGUAUAGU-3′
UUCGAGGUAGAUCCAACAUAU
4 nt 5′ central mismatched 2′-O-methyl target : siRNA
3′-UUCCAACUCCAAGAACCAACAUAUCACUUAA-5′
5′-UGAGGUAGUAGGUUGUAUAGU-3′
UUACUCCAUCAUCCAACAUAU
4 nt 3′ central mismatched 2′-O-methyl target : siRNA
3′-UUCCAACUCCAUCAAGGUACAUAUCACUUCU-5′
5′-UGAGGUAGUAGGUUGUAUAGU-3′
UUACUCCAUCAUCCAACAUAU
4 nt 3′ mismatched 2′-O-methyl target : siRNA
3′-UUCCAACUCCAUCAUCCAACAUCAACCUUCU-5′
5′-UGAGGUAGUAGGUUGUAUAGU-3′
UUACUCCAUCAUCCAACAUAU
7 nt 3′ mismatched 2′-O-methyl target : siRNA
3′-UUCCAACUCCAUCAUCCAGAACCAACCUUCU-5′
5′-UGAGGUAGUAGGUUGUAUAGU-3′
UUACUCCAUCAUCCAACAUAU
8 nt 3′ mismatched 2′-O-methyl target : siRNA
3′-UUCCAACUCCAUCAUCCAACAUAUCACUUCU-bi-5′
5′-UGAGGUAGUAGGUACAUGCAG-3′
UUCCUCCAUCAUCCAAGUACG

Figure 5c

TABLE 1

Table 1 Kinetic analysis of RISC

Summary of kinetic data from the analysis in Figure 17A. For comparison, the K_M and k_{cat} values of four well studied protein enzymes are provided[43,44]. K_M and k_{cat} ± error of fit are reported.

Mismatches, position	K_M (nM)	V_{max} (nM s^{-1})	[RISC] (nM)	k_{cat} (s^{-1})	k_{cat} K_M^{-1} (nM^{-1} s^{-1})	fold change, k_{cat} K_M^{-1}
none	8.4 ± 1.6	0.0071	1	7.1×10^{-3}	8.4×10^{-4}	1.00
three nt 3′	2.7 ± 0.6	0.0022	2	1.1×10^{-3}	3.8×10^{-4}	0.46
five nt 3′	6.0 ± 1.8	0.0054	2	2.7×10^{-4}	4.5×10^{-5}	0.05
three nt 5′	4.7 ± 1.3	0.0063	2	3.2×10^{-3}	6.7×10^{-4}	0.80

Reference enzymes	K_M (nM)	k_{cat} (s^{-1})	k_{cat} K_M^{-1} (nM^{-1} s^{-1})	k_{cat} K_M^{-1} relative to RISC
Urease (ref 43)	2.5×10^{7}	1×10^{4}	4.0×10^{-4}	0.47
Fumarase (ref 43)	5.0×10^{3}	8×10^{2}	1.6×10^{-1}	190
Catalase (ref 43)	2.5×10^{7}	1×10^{7}	4.0×10^{-1}	8940
RNase H1 (ref 44)	3.8×10^{1}	5×10^{2}	1.3×10^{-3}	0.03